

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-556-178-5.rag.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103254_us-09-556-178-5.rag.

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GenCore version 6.3
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OM protein - protein search, using sw model

Run on: December 14, 2010, 11:22:17 ; Search time 37 Seconds
(without alignments)
5898.160 Million cell updates/sec

Title: US-09-556-178-5
Perfect score: 882
Sequence: 1 MEALILEPSLYTVKAILILD.....QTVSQVLQSAKEQIKWSLLR 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6395994 seqs, 1224146475 residues

Total number of hits satisfying chosen parameters: 6395994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_201023:*
1: geneseq1:*
2: geneseq2:*
3: geneseq3:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	882	100.0	177	1 AAY49960	Aay49960 Human ves
2	882	100.0	177	1 AAB03815	Aab03815 Human ves
3	882	100.0	177	1 AAB03789	Aab03789 Human cap
4	882	100.0	177	1 ADO23737	Ado23737 COPI coat
5	882	100.0	177	2 AEJ65021	Aej65021 Liver can
6	882	100.0	177	3 AYI11804	Ayil1804 Human coa
7	845	95.8	177	1 ADO57263	Ado57263 Kidney de
8	673	76.3	210	1 AAY31641	Aay31641 Human tra
9	673	76.3	210	1 ADO23725	Ado23725 COPI coat
10	673	76.3	210	3 AYI11805	Ayil1805 Human coa
11	671	76.1	137	1 AAG01470	Aag01470 Human sec
12	580	65.8	185	1 ADO21857	Ado21857 Human ves
13	564.5	64.0	160	1 ABB60295	Abb60295 Drosophil
14	564.5	64.0	160	2 AFB87634	Afb87634 Fruit fly

15	507.5	57.5	181	2	ARO36046	Aro36046 Soybean c
16	507.5	57.5	181	2	ARO37763	Aro37763 Soybean c
17	507.5	57.5	181	3	AXJ10909	Axj10909 Heteroder
18	507.5	57.5	181	3	AXJ09192	Axj09192 Heteroder
19	493.5	56.0	175	2	ADY65214	Ady65214 S. mansoni
20	441.5	50.1	154	2	ARO39451	Aro39451 Soybean c
21	441.5	50.1	154	3	AXJ12597	Axj12597 Heteroder
22	440	49.9	99	1	AAB54324	Aab54324 Human pan
23	394	44.7	179	2	AFQ47080	Afq47080 Glycine m
24	386	43.8	177	2	ARM90905	Arm90905 Arabidops
25	386	43.8	177	2	ARM94661	Arm94661 Arabidops
26	379	43.0	177	2	ARB02835	Arb02835 Cotton pr
27	375.5	42.6	180	1	AFP84367	Afp84367 Glycine m
28	373	42.3	182	2	ARL84894	Ar184894 Maize pla
29	371	42.1	182	1	AAG35416	Aag35416 Zea mays
30	371	42.1	182	2	ALJ76006	Alj76006 Plant pro
31	371	42.1	182	2	AFC59274	Afc59274 Maize ami
32	371	42.1	182	2	ARM13352	Arm13352 Zea mays
33	371	42.1	182	3	AYF39857	Ayf39857 Plant pol
34	371	42.1	206	1	ADX78919	Adx78919 Plant ful
35	371	42.1	206	2	ANO11441	Ano11441 Zea mays
36	371	42.1	225	1	ADY23237	Ady23237 Plant ful
37	371	42.1	225	2	ANO34177	Ano34177 Zea mays
38	368	41.7	179	1	AAG38559	Aag38559 Arabidops
39	368	41.7	179	2	ALJ80333	Alj80333 Plant pro
40	368	41.7	179	2	ARN03104	Arn03104 Arabidops
41	368	41.7	225	2	ARN03103	Arn03103 Arabidops
42	364	41.3	182	2	ARM52453	Arm52453 Glycine m
43	359	40.7	177	1	ADT60317	Adt60317 Plant pol
44	359	40.7	177	2	AFC50108	Afc50108 Wheat ami
45	359	40.7	177	2	AJG83201	Ajg83201 Triticum

ALIGNMENTS

RESULT 1

AAY49960

ID AAY49960 standard; protein; 177 AA.

XX

AC AAY49960;

XX

DT 15-JUN-2007 (revised)

DT 04-FEB-2000 (first entry)

XX

DE Human vesicle trafficking protein 3.

XX

KW Human; vesicle trafficking protein; VTP-1; VTP-2; VTP-3; apoptosis;

KW cancer; inflammation; BOND_PC; coatomer protein complex, subunit zeta 1;

KW CGI-120 protein; coatomer protein complex, subunit zeta 1 [Homo sapiens];

KW COPZ1; COPZ; CGI-120; zetal-COP; subunit zeta;

KW nonclathrin coat protein zetal-COP;

KW coatomer protein complex, subunit zeta 1 [Mus musculus]; D4Ert2360e;

KW 5930435A22Rik; AA407760; MGC118060;

KW similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);

KW LOC609925; LOC607013;

KW coatomer protein complex, subunit zeta 1, isoform CRA_a;

KW coatomer protein complex, subunit zeta 1, isoform CRA_a [Homo sapiens];

KW unnamed protein product; unnamed protein product [Mus musculus];

KW hypothetical protein; hypothetical protein [Pongo pygmaeus]; HSPC181;

KW HSPC181 [Homo sapiens]; z-cop; z-cop [Homo sapiens];

KW Coatomer protein complex, subunit zeta 1 [Homo sapiens];

KW CGI-120 protein [Homo sapiens]; zetal-COP [Homo sapiens];

KW unnamed protein product [Macaca fascicularis];

KW Coatomer protein complex, subunit zeta 1 [Mus musculus];

KW nonclathrin coat protein zeta-COP;

KW nonclathrin coat protein zeta-COP [Mus musculus]; Copz1 protein;

KW Copz1 protein [Mus musculus]; G05783; G06886; G06888; G06890; G06891;
 KW G016020; G030126; G030662; G05198; G08565.
 XX
 OS Homo sapiens.
 XX
 PN US5989859-A.
 XX
 PD 23-NOV-1999.
 XX
 PF 07-NOV-1997; 97US-00967364.
 XX
 PR 07-NOV-1997; 97US-00967364.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Bandman O, Guegler KJ, Corley NC, Lal P, Shah P;
 XX
 DR WPI; 2000-022782/02.
 DR N-PSDB; AAZ35835.
 DR PC:NCBI; gi7706337.
 DR PC:SWISSPROT; P61923, P61924, Q5R5F2.
 DR PC:BIND; 54453.
 XX
 PT Novel vesicle trafficking proteins used in the diagnosis, prevention, and
 PT treatment of inflammation or cancer.
 XX
 PS Claim 9; Fig 7; 55pp; English.
 XX
 CC The present sequence represents the human vesicle trafficking protein
 CC designated VTP-3. VTPs can be used in a method for preventing or treating
 CC disease associated with an increase in apoptosis. The method can treat
 CC diseases such as cancer and inflammation, by administering a VTP
 CC antagonist
 CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 177 AA;

Query Match 100.0%; Score 882; DB 1; Length 177;
 Best Local Similarity 100.0%;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVKEQKAFKKNIFNKTHTDSEIA	60
Db	1	MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVKEQKAFKKNIFNKTHTDSEIA	60
Qy	61	LLEGLTVVYKSSIDLIFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG	120
Db	61	LLEGLTVVYKSSIDLIFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG	120
Qy	121	LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR	177
Db	121	LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR	177

RESULT 2

AAB03815

ID AAB03815 standard; protein; 177 AA.

XX

AC AAB03815;

XX

DT 15-JUN-2007 (revised)

DT 13-OCT-2000 (first entry)

XX

DE Human vesicle trafficking protein-3 (VTP-3) amino acid sequence.

XX

KW Vesicle trafficking protein; VTP-3; human; cancer; inflammation; asthma;
 KW foetal development; Crohn's disease; diabetes; multiple sclerosis;
 KW rheumatoid arthritis; infection; ulcerative colitis; proliferation;
 KW irritable bowel syndrome; apoptosis; AIDS; Alzheimer's disease;
 KW Parkinson's disease; osteoporosis; wasting disorder; BOND_PC;
 KW coatomer protein complex, subunit zeta 1; CGI-120 protein;
 KW coatomer protein complex, subunit zeta 1 [Homo sapiens]; COP21; COP2;
 KW CGI-120; zetal-COP; subunit zeta; nonclathrin coat protein zetal-COP;
 KW coatomer protein complex, subunit zeta 1 [Mus musculus]; D4Erd360e;
 KW 5930435A22Rik; AA407760; MGC118060;
 KW similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);
 KW LOC609925; LOC607013;
 KW coatomer protein complex, subunit zeta 1, isoform CRA_a;
 KW coatomer protein complex, subunit zeta 1, isoform CRA_a [Homo sapiens];
 KW unnamed protein product; unnamed protein product [Mus musculus];
 KW hypothetical protein; hypothetical protein [Pongo pygmaeus]; HSPC181;
 KW HSPC181 [Homo sapiens]; z-cop; z-cop [Homo sapiens];
 KW Coatomer protein complex, subunit zeta 1 [Homo sapiens];
 KW CGI-120 protein [Homo sapiens]; zetal-COP [Homo sapiens];
 KW unnamed protein product [Macaca fascicularis];
 KW Coatomer protein complex, subunit zeta 1 [Mus musculus];
 KW nonclathrin coat protein zeta-COP;
 KW nonclathrin coat protein zeta-COP [Mus musculus]; Cop21 protein;
 KW Cop21 protein [Mus musculus]; G05783; G06886; G06889; G06891;
 KW G016020; G030126; G030662; G05198; G08565.

XX
 OS Homo sapiens.

XX
 PN US6071703-A.

XX
 PD 06-JUN-2000.

XX
 PF 04-AUG-1999; 99US-00368408.

XX
 PR 07-NOV-1997; 97US-00967364.

XX
 PA (INCY-) INCYTE PHARM INC.

XX
 PI Guegler KJ, Shah P, Corley NC, Bandman O, Lal P;

XX
 DR WPI; 2000-422079/36.

DR N-PSDB; AAA59875.

DR PC:NCBI; gi7706337.

DR PC:SWISSPROT; P61923, P61924, Q5R5F2.

DR PC:BIND; 54453.

XX
 PT Identifying polynucleotides encoding vesicle trafficking proteins (VTP)

PT for treating and preventing e.g. inflammation, by detecting a

PT hybridization complex of a nucleic acid from a sample and a

PT polynucleotide encoding a VTP.

XX
 PS Claim 1; Fig 7; 55pp; English.

XX
 CC This sequence represents a human vesicle trafficking protein (VTP-3)
 CC amino acid sequence. VTP-3 encoding cDNA was isolated from an aortic
 CC tissue cDNA library (HEAONOT03). VTP-3 has structural and chemical
 CC homology with a subunit of cow coatomer protein, zeta COP. The present
 CC invention relates to a method for detecting human VTP encoding
 CC polynucleotide sequences and includes nucleotide and protein sequences
 CC for human VTP-1, VTP-2 and VTP-3. Northern analysis of VTP-1, 2, and 3
 CC shows that their expression is associated with cancer, inflammation and
 CC foetal/infant development. The method of the invention is useful for
 CC screening and identifying a polynucleotide encoding a human VTP, which
 CC may be used for the diagnosis, prevention, or treatment of inflammation
 CC associated disorder, e.g. asthma, Crohn's disease, diabetes, multiple
 CC sclerosis, rheumatoid arthritis, infections, ulcerative colitis and
 CC irritable bowel syndrome. Other diseases and disorders identified,

CC prevented or treated with polynucleotide sequences encoding VTP include
 CC those associated with cell proliferation or apoptosis, such as AIDS,
 CC Alzheimer's disease, Parkinson's disease, osteoporosis, wasting diseases
 CC and cancer
 CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 177 AA;

Query Match 100.0%; Score 882; DB 1; Length 177;
 Best Local Similarity 100.0%;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVSKQKAFKFNIFNKTHTRDSEIA 60
 Db 1 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVSKQKAFKFNIFNKTHTRDSEIA 60

Qy 61 LLEGLTVVYKSSIDLIFYFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 120
 Db 61 LLEGLTVVYKSSIDLIFYFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 120

Qy 121 LFLAVDEIVDGGVILESDPQQVVRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
 Db 121 LFLAVDEIVDGGVILESDPQQVVRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177

RESULT 3

AAB03789

ID AAB03789 standard; protein; 177 AA.
 XX
 AC AAB03789;
 XX
 DT 15-JUN-2007 (revised)
 DT 26-OCT-2000 (first entry)
 XX
 DE Human capsid protein zeta-COP amino acid sequence.
 XX
 KW Human; capsid-protein; zeta-COP; BOND_PC;
 KW coatomer protein complex, subunit zeta 1; CGI-120 protein;
 KW coatomer protein complex, subunit zeta 1 [Homo sapiens]; COP21; COP2;
 KW CGI-120; zeta1-COP; subunit zeta; nonclathrin coat protein zeta1-COP;
 KW coatomer protein complex, subunit zeta 1 [Mus musculus]; D4Erd360e;
 KW 5930435A22Rik; AA407760; MGC118060;
 KW similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);
 KW LOC609925; LOC607013;
 KW coatomer protein complex, subunit zeta 1, isoform CRA_a;
 KW coatomer protein complex, subunit zeta 1, isoform CRA_a [Homo sapiens];
 KW unnamed protein product; unnamed protein product [Mus musculus];
 KW hypothetical protein; hypothetical protein [Pongo pygmaeus]; HSPC181;
 KW HSPC181 [Homo sapiens]; z-cop; z-cop [Homo sapiens];
 KW Coatomer protein complex, subunit zeta 1 [Homo sapiens];
 KW CGI-120 protein [Homo sapiens]; zeta1-COP [Homo sapiens];
 KW unnamed protein product [Macaca fascicularis];
 KW Coatomer protein complex, subunit zeta 1 [Mus musculus];
 KW nonclathrin coat protein zeta-COP;
 KW nonclathrin coat protein zeta-COP [Mus musculus]; Cop21 protein;
 KW Cop21 protein [Mus musculus]; GO5783; GO6886; GO6888; GO6890; GO6891;
 KW GO16020; GO30126; GO30662; GO5198; GO8565.
 XX
 OS Homo sapiens.
 XX
 PN CN1248624-A.
 XX
 PD 29-MAR-2000.
 XX
 PF 22-SEP-1998; 98CN-00119744.

```

XX
PR    22-SEP-1998;    98CN-00119744.
XX
PA    (XINH-) XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.
XX
PI    Yu L,  Tu Q,  Fu Q;
XX
DR    WPI; 2000-431993/38.
DR    N-PSDB; AAA59847.
DR    PC:NCBI; gi7706337.
DR    PC:SWISSPROT; P61923, P61924, Q5R5F2.
DR    PC:BIND; 54453.
XX
PT    Novel human capsid protein subunit coding sequence.
XX
PS    Claim 2; Fig 2; 21pp; Chinese.
XX
CC    This invention relates to a human gene encoding a capsid protein zeta
CC    subunit (zeta-COP). The invention also relates to a zeta-COP protein
CC    sequence. The present sequence represents the human zeta-COP protein
CC    sequence
CC
CC    Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC    information from BOND.
XX
SQ    Sequence 177 AA;

Query Match          100.0%; Score 882; DB 1; Length 177;
Best Local Similarity 100.0%;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVKEQKAFAEKNIFNKTHTRDSEIA 60
Db      1 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVKEQKAFAEKNIFNKTHTRDSEIA 60

Qy      61 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 120
Db      61 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 120

Qy      121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
Db      121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177

```

RESULT 4

ADO23737

ID ADO23737 standard; protein; 177 AA.

XX

AC ADO23737;

XX

DT 15-JUN-2007 (revised)

DT 01-JUL-2004 (first entry)

XX

DE COPI coatomer protein, SEQ ID 26.

XX

KW Cytostatic; nuclear envelope breakdown; nuclear pore protein; Nup153;

KW COPI coatomer complex; cancer; BOND_PC;

KW coatomer protein complex, subunit zeta 1; CGI-120 protein;

KW coatomer protein complex, subunit zeta 1 [Homo sapiens]; COPZ1; COPZ;

KW CGI-120; zeta1-COP; subunit zeta; nonclathrin coat protein zeta1-COP;

KW coatomer protein complex, subunit zeta 1 [Mus musculus]; D4Ertcd360e;

KW 5930435A22Rik; AA07760; MGC118060;

KW similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);

KW LOC609925; LOC607013;

KW coatomer protein complex, subunit zeta 1, isoform CRA_a;

KW coatomer protein complex, subunit zeta 1, isoform CRA_a [Homo sapiens];

KW unnamed protein product; unnamed protein product [Mus musculus];

KW hypothetical protein; hypothetical protein [Pongo pygmaeus]; HSPC181;
 KW HSPC181 [Homo sapiens]; z-cop; z-cop [Homo sapiens];
 KW Coatomer protein complex, subunit zeta 1 [Homo sapiens];
 KW CGI-120 protein [Homo sapiens]; zeta1-COP [Homo sapiens];
 KW unnamed protein product [Macaca fascicularis];
 KW Coatomer protein complex, subunit zeta 1 [Mus musculus];
 KW nonclathrin coat protein zeta-COP;
 KW nonclathrin coat protein zeta-COP [Mus musculus]; Copz1 protein;
 KW Copz1 protein [Mus musculus].
 XX
 OS Unidentified.
 XX
 PN WO2004027381-A2.
 XX
 PD 01-APR-2004.
 XX
 PF 17-SEP-2003; 2003WO-US029267.
 XX
 PR 17-SEP-2002; 2002US-0411248P.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 PI Ulmann KS, Liu J, Prunuske A, Dimaano C;
 XX
 DR WPI; 2004-340314/31.
 DR N-PSDB; ADO23736.
 DR PC:NCBI; gi4929709.
 DR PC:SWISSPROT; P61923, P61924, Q5R5F2.
 DR PC:BIND; 54453.
 XX
 PT New composition comprising a molecule that inhibits nuclear envelope
 PT breakdown, useful in treating cancer, e.g. lymphoma, sarcoma or glioma.
 XX
 PS Claim 22; SEQ ID NO 26; 180pp; English.
 XX
 CC The present invention relates to a composition comprising a molecule that
 CC inhibits nuclear envelope breakdown by interfering with the interaction
 CC between nuclear pore protein Nup153 and COPI coatomer complex. The
 CC composition is useful in treating, inhibiting or preventing cancer, e.g.
 CC lymphoma, leukaemia, mycosis fungoide, carcinoma, adenocarcinoma,
 CC sarcoma, glioma, blastoma, neuroblastoma, plasmacytoma, histiocytoma,
 CC melanoma, adenoma, hypoxic tumour, myeloma, AIDS-related lymphoma or AIDS
 CC -related sarcoma or metastatic, bladder, brain or nervous system cancer,
 CC glioblastoma or ovarian, skin or liver cancer, squamous cell carcinomas
 CC of the mouth, throat, larynx, and lung or colon, cervical, breast,
 CC epithelial, renal, genitourinary or pulmonary cancer, oesophageal
 CC carcinoma, head and neck carcinoma or haematopoietic, testicular,
 CC colorectal, prostatic or pancreatic cancer. The present sequence was used
 CC to illustrate the invention.
 CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 177 AA;

Query Match 100.0%; Score 882; DB 1; Length 177;
 Best Local Similarity 100.0%;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVSKQKAFEKNIFNFKTHRTDSEIA	60
Db	1	MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVSKQKAFEKNIFNFKTHRTDSEIA	60
Qy	61	LLEGLTVVYKSSIDLFFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG	120
Db	61	LLEGLTVVYKSSIDLFFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG	120

Qy 121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVS QVLQSAKEQIKWSLLR 177
 |||
 Db 121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVS QVLQSAKEQIKWSLLR 177

RESULT 5

AEJ65021

ID AEJ65021 standard; protein; 177 AA.

XX

AC AEJ65021;

XX

DT 15-JUN-2007 (revised)

DT 05-OCT-2006 (first entry)

XX

DE Liver cancer associated protein SEQ ID NO 63.

XX

KW protein production; recombinant DNA; liver tumor; cytostatic; neoplasm;

KW gastrointestinal disease; BOND_PC;

KW coatomer protein complex, subunit zeta 1; CGI-120 protein;

KW coatomer protein complex, subunit zeta 1 [Homo sapiens]; COPZ1; COPZ;

KW CGI-120; zetal-COP; subunit zeta; nonclathrin coat protein zetal-COP;

KW coatomer protein complex, subunit zeta 1 [Mus musculus]; D4Erd360e;

KW 5930435A22Rik; AA407760; MGC118060;

KW similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);

KW LOC609925; LOC607013;

KW coatomer protein complex, subunit zeta 1, isoform CRA_a;

KW coatomer protein complex, subunit zeta 1, isoform CRA_a [Homo sapiens];

KW unnamed protein product; unnamed protein product [Mus musculus];

KW hypothetical protein; hypothetical protein [Pongo pygmaeus]; HSPC181;

KW HSPC181 [Homo sapiens]; z-cop; z-cop [Homo sapiens];

KW Coatomer protein complex, subunit zeta 1 [Homo sapiens];

KW CGI-120 protein [Homo sapiens]; zetal-COP [Homo sapiens];

KW unnamed protein product [Macaca fascicularis];

KW Coatomer protein complex, subunit zeta 1 [Mus musculus];

KW nonclathrin coat protein zeta-COP;

KW nonclathrin coat protein zeta-COP [Mus musculus]; Copz1 protein;

KW Copz1 protein [Mus musculus]; GO5783; GO6886; GO6888; GO6890; GO6891;

KW GO16020; GO30126; GO30662; GO5198; GO8565.

XX

OS Homo sapiens.

XX

PN CN1618808-A.

XX

PD 25-MAY-2005.

XX

PF 21-NOV-2003; 2003CN-10108764.

XX

PR 21-NOV-2003; 2003CN-10108764.

XX

PA (SHAN-) SHANGHAI HUMAN GENOME RES CENT.

XX

PI Zhu Z, Han Z;

XX

DR WPI; 2005-640540/66.

DR SWISSPROT; Q9Y3C3.

DR PC:NCBI; gi7706337.

DR PC:SWISSPROT; P61923, P61924, Q5R5F2.

DR PC:BIND; 54453.

XX

PT Liver cancer related protein and its coding sequence and use.

XX

PS Claim 1; SEQ ID NO 63; 26pp; Chinese.

XX

CC The invention describes a novel liver cancer associated protein, the polynucleotide for coding it, the process for preparing said protein by recombination, and the application of said polynucleotide. This is the amino acid sequence of a liver cancer associated protein.

CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 177 AA;

Query Match 100.0%; Score 882; DB 2; Length 177;
Best Local Similarity 100.0%;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEALILEPSLYTVKAILILDNDGDRLEFAKYDDTYPVSKQKAFKFNIFNKTHTDSEIA 60
|
Db 1 MEALILEPSLYTVKAILILDNDGDRLEFAKYDDTYPVSKQKAFKFNIFNKTHTDSEIA 60

Qy 61 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
|
Db 61 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy 121 LFLAVDEIVDGGVILESDPQQVVRVALRGEDVPLTEQTVSQVLQSAKEIKWSLLR 177
|
Db 121 LFLAVDEIVDGGVILESDPQQVVRVALRGEDVPLTEQTVSQVLQSAKEIKWSLLR 177

RESULT 6

AY11804

ID AY11804 standard; protein; 177 AA.

XX
AC AY11804;
XX
DT 28-OCT-2010 (first entry)
XX
DE Human coatomer subunit zeta-1 protein, SEQ ID 29.
XX
KW Bio-nanoparticle element; Coatomer subunit zeta-1; nanotechnology;
KW BOND_PC; coatomer protein complex, subunit zeta 1; CGI-120 protein;
KW COP21; COP2; CGI-120; zetal-COP; subunit zeta;
KW nonclathrin coat protein zetal-COP; D4Ert360e; 5930435A22Rik; AA407760;
KW MG118060;
KW similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);
KW LOC609925; LOC607013; similar to CGI-120 protein;
KW PREDICTED: similar to CGI-120 protein [Equus caballus]; LOC100064590;
KW Cop21_predicted;
KW similar to Coatomer subunit zeta-1 (Zeta-1-coat protein) (Zeta-1 COP);
KW LOC100156765; Coatomer subunit zeta-1; DKFZp469A0331;
KW coatomer protein complex, subunit zeta 1, isoform CRA_a;
KW unnamed protein product; hypothetical protein; HSPC181; z-cop;
KW nonclathrin coat protein zeta-COP; Cop21 protein; G05783; G06886; G06888;
KW G06890; G06891; G016020; G030126; G030662; G05198; G08565.
XX
OS Homo sapiens.
XX
PN US2010226856-A1.
XX
PD 09-SEP-2010.
XX
PF 06-MAR-2009; 2009US-00399906.
XX
PR 06-MAR-2009; 2009US-00399906.
XX
PA (VITA/) VITALIANO F.
PA (VITA/) VITALIANO G.
XX
PI Vitaliano F, Vitaliano G;
XX
DR WPI; 2010-L54477/62.
DR SWISSPROT; P61923.
DR PC:NCBI; gi7706337.


```

Qy      121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVS QVLQSAKEQIKWSLLR 177
        |||
Db      121 LFLAVDEIVDGGVILESDPQQVVHRVALRGDDVPLTEQTVTQVLQSAKEQIKWSLLR 177

```

RESULT 8

AAY31641

ID AAY31641 standard; protein; 210 AA.

XX

AC AAY31641;

XX

DT 02-NOV-1999 (first entry)

XX

DE Human transport-associated protein-3 (TRANP-3).

XX

KW Transport-associated protein; TRANP; nuclear pore; nuclear transport;
 KW vesicle trafficking; cancer; cystic fibrosis; multidrug resistance;
 KW hypercholesterolaemia; diagnosis; treatment.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site

44

FT /note= "O-phosphorylated by tyrosine kinase"

FT Modified-site

45

FT /note= "O-phosphorylated by protein kinase C"

FT Modified-site

55

FT /note= "Amidation site"

FT Modified-site

70

FT /note= "O-phosphorylated by casein kinase II or protein
kinase C"

FT Modified-site

83

FT /note= "N-glycosylated"

FT Modified-site

85

FT /note= "O-phosphorylated by protein kinase C"

FT Modified-site

86

FT /note= "O-phosphorylated by casein kinase II"

FT Modified-site

88

FT /note= "O-phosphorylated by casein kinase II"

FT Modified-site

111

FT /note= "O-phosphorylated by tyrosine kinase"

FT Modified-site

115

FT /note= "O-phosphorylated by casein kinase II"

FT Modified-site

199

FT /note= "O-phosphorylated by casein kinase II or protein
kinase C"

XX

PN W09941373-A2.

XX

PD 19-AUG-1999.

XX

PF 05-FEB-1999; 99WO-US002527.

XX

PR 11-FEB-1998; 98US-00021764.

XX

PA (INCY-) INCYTE PHARM INC.

XX

PI Au-Young J, Hillman JL, Lal P, Guegler KJ, Corley NC, Yue H;

PI Bandman O, Baughn MR;

XX

DR WPI; 1999-508646/42.

DR N-PSDB; AAZ11733.

XX

PT Human TRANP coding sequences, used to treat transport disorders and
 PT cancer.

XX

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103255_us-09-556-178-5 rpr.

GenCore version 6.3
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OM protein - protein search, using sw model

Run on: December 14, 2010, 11:24:11 ; Search time 2 Seconds
(without alignments)
7139.284 Million cell updates/secTitle: US-09-556-178-5
Perfect score: 882
Sequence: 1 MEALILEPRLTYNKAILED.....QTVSQVQLGSAEDQINWLLR 177Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summariesDatabase : PIR_80:
1: pir1:
2: pir2:
3: pir3:
4: pir4:
SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	875	99.2	177	2 A49465	coatamer zeta chain
2	499	56.6	184	2 T23002	hypothetical prote
3	344	35.0	162	2 C96635	probable coatamer
4	308	34.9	189	2 S52521	coatamer protein z
5	299.5	34.0	190	2 T41417	coatamer zeta subu
6	267	30.3	153	2 T01831	hypothetical prote
7	141.5	16.0	145	2 T08407	clathrin coat asse
8	118	13.4	143	2 B84581	probable clathrin
9	117	13.3	446	2 C39466	clathrin coat asse
10	116	11.2	144	2 S56796	ADP19 protein homo
11	112.5	12.8	141	2 C71605	clathrin coat asse
12	108	12.2	157	2 T31801	hypothetical prote
13	106.5	12.1	143	2 T40635	clathrin coat asse
14	99	11.2	165	2 S62563	adaptin complex sm
15	98	11.1	1472	2 S67195	probable membrane
16	97.5	11.1	441	2 B49837	clathrin-associate
17	90.5	10.3	214	2 S51405	synaptobrevin SN2
18	90	10.2	1271	2 T08607	hypothetical prote
19	88.5	10.0	290	2 C96911	transcription regu
20	87.5	9.9	475	2 S63590	clathrin-associate
21	86	9.8	158	2 A40535	clathrin-associate
22	86	9.8	161	2 E84551	clathrin assembly
23	86	9.8	162	2 T09116	probable clathrin-
24	85.5	9.7	663	2 B70460	exonuclease ABC c
25	85.5	9.7	699	2 T18984	hypothetical prote
26	85	9.6	380	2 D64129	probable S-amino-7
27	84.5	9.6	439	2 J78378	naturase-like prot
28	84.5	9.6	863	2 B72344	tRNA nucleotidyl t
29	84	9.5	132	2 T02991	clathrin coat asse
30	84	9.5	142	2 T15957	hypothetical prote
31	83.5	9.5	412	2 E97736	mitochondrial prot
32	83	9.4	142	2 B40935	clathrin-associate
33	83	9.4	156	2 B37757	clathrin-associate
34	83	9.4	410	2 S64451	hypothetical prote
35	83	9.4	896	2 T47645	centromere protein
36	82.5	9.4	324	2 C90492	hypothetical prote
37	82.5	9.4	569	1 D64215	conserved hypoth
38	82.5	9.4	909	2 A23114	exonuclease ABC c
39	82.5	9.4	1104	2 B16713	CTPase-activating
40	82	9.3	416	2 D70347	cell division prot
41	82	9.3	659	2 S81134	probable N-acetyl
42	82	9.3	686	2 T23721	hypothetical prote
43	82	9.3	725	2 G90555	vach-like (shigell
44	82	9.3	803	1 E70041	probable copper-tr
45	82	9.3	1130	2 T21134	hypothetical prote

ALIGNMENTS

RESULT 1
A49465
coatamer zeta chain - bovine
C|Species: Bos primigenius taurus (cattle)
C|Status: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C|Accession: A49465
R|Kuge, G.; Hara-Kuge, S.; Orel, L.; Ravazzola, M.; Amherdt, M.; Tanigawa, G.; Wieland, F.T.; Rothman, J.E.
J. Cell Biol. 121, 177-173 (1993)
A|Title: zeta-COP, a subunit of coatamer, is required for COP-coated vesicle assembly.
A|Reference numbers: A49465; MUID:94103328; PMID:8276893
A|Accession: A49465
A|Status: preliminary
A|Molecule type: mRNA

<http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb227b&ItemName=2010...> 1/10/11

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-556-178- 5.rup.

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OM protein - protein search, using sw model

Run on: December 14, 2010, 11:23:42 ; Search time 96 Seconds
(without alignments)
7637.199 Million cell updates/sec

Title: US-09-556-178-5
Perfect score: 882
Sequence: 1 MEALILEPSLYTVKAILILD.....QTVSQVLQSAKEQIKWSLLR 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 12869322 seqs, 4158259533 residues

Total number of hits satisfying chosen parameters: 12869322

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_201011:*
1: uniprot_sprot:*
2: uniprot_trembl:*
SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	882	100.0	177	1	COPZ1_HUMAN	P61923 RecName: Fu
2	882	100.0	177	1	COPZ1_MOUSE	P61924 RecName: Fu
3	882	100.0	177	1	COPZ1_PONAB	Q5r5f2 RecName: Fu
4	882	100.0	177	2	D4A8T3_RAT	D4a8t3 SubName: Fu
5	882	100.0	177	2	Q542M2_MOUSE	Q542m2 SubName: Fu
6	878	99.5	177	1	COPZ1_BOVIN	P35604 RecName: Fu
7	877	99.4	177	2	Q53FU3_HUMAN	Q53fu3 SubName: Fu
8	847	96.0	177	2	Q28HL1_XENTR	Q28hl1 SubName: Fu
9	846	95.9	177	2	A0AUT9_XENLA	A0aut9 SubName: Fu
10	846	95.9	187	2	Q801P3_XENLA	Q801p3 SubName: Fu
11	845	95.8	177	2	Q91B48_DANRE	Q91b48 SubName: Fu
12	843	95.6	177	2	Q6GQG0_XENLA	Q6gqq0 SubName: Fu
13	842	95.5	177	2	Q7SXH1_DANRE	Q7sxh1 SubName: Fu
14	836	94.8	177	2	C3KJY4_ANOFI	C3k jy4 SubName: Fu
15	832	94.3	177	2	B5X5K5_SALSA	B5x5k5 SubName: Fu

16	832	94.3	179	2	C1BY80_ESOLU	C1by80	SubName: Fu
17	828	93.9	177	2	B5X8E4_SALSA	B5x8e4	SubName: Fu
18	828	93.9	177	2	C1BH15_ONCMY	C1bh15	SubName: Fu
19	828	93.9	177	2	C3KJ46_ANOFI	C3kj46	SubName: Fu
20	825	93.5	177	2	B9EM01_SALSA	B9em01	SubName: Fu
21	819	92.9	175	2	C1BFE7_ONCMY	C1bfe7	SubName: Fu
22	815	92.4	174	2	B5X954_SALSA	B5x954	SubName: Fu
23	814	92.3	177	2	C1BH82_ONCMY	C1bh82	SubName: Fu
24	813	92.2	163	2	Q8R3M1_MOUSE	Q8r3m1	SubName: Fu
25	810	91.8	177	2	B5XDE2_SALSA	B5xde2	SubName: Fu
26	745.5	84.5	154	2	B4DDX8_HUMAN	B4ddx8	SubName: Fu
27	701.5	79.5	173	2	Q9IB47_DANRE	Q9ib47	SubName: Fu
28	692	78.5	189	2	Q6DKF5_DANRE	Q6dkf5	SubName: Fu
29	683.5	77.5	229	2	C3XTB6_BRAFL	C3xtb6	SubName: Fu
30	673.5	76.4	178	2	B9EQ95_SALSA	B9eq95	SubName: Fu
31	673	76.3	179	2	B9EPB0_SALSA	B9epb0	SubName: Fu
32	673	76.3	210	1	COPZ2_HUMAN	Q9p299	RecName: Fu
33	667	75.6	205	1	COPZ2_MOUSE	Q9jhh9	RecName: Fu
34	666.5	75.6	178	2	C1BHL1_ONCMY	C1bhl1	SubName: Fu
35	664	75.3	203	2	C1BFJ5_ONCMY	C1bfj5	SubName: Fu
36	663	75.2	185	2	Q9CTG7_MOUSE	Q9ctg7	SubName: Fu
37	649	73.6	156	2	Q6P383_XENTR	Q6p383	SubName: Fu
38	625.5	70.9	178	2	E0VA85_PEDHC	E0va85	SubName: Fu
39	623	70.6	183	2	A7S1D0_NEMVE	A7s1d0	SubName: Fu
40	621.5	70.5	177	2	Q16K41_AEDAE	Q16k41	SubName: Fu
41	620.5	70.4	177	2	B0W863_CULQU	B0w863	SubName: Fu
42	620.5	70.4	182	2	D6WPS8_TRICA	D6wps8	SubName: Fu
43	620	70.3	181	2	Q16K40_AEDAE	Q16k40	SubName: Fu
44	619.5	70.2	178	2	C4WUX3_ACYPI	C4wux3	SubName: Fu
45	612.5	69.4	177	2	Q7Q5C2_ANOGA	Q7q5c2	SubName: Fu

ALIGNMENTS

RESULT 1

COPZ1_HUMAN

ID COPZ1_HUMAN Reviewed; 177 AA.
AC P61923; Q549N6; Q9Y3C3;
DT 07-JUN-2004, integrated into UniProtKB/Swiss-Prot.
DT 07-JUN-2004, sequence version 1.
DT 05-OCT-2010, entry version 66.
DE RecName: Full=Coatomer subunit zeta-1;
DE AltName: Full=Zeta-1-coat protein;
DE Short=Zeta-1 COP;
GN Name=COPZ1; Synonyms=COPZ; ORFNames=CGI-120, HSPC181;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=20512057; PubMed=11056392;
RA Futatsumori M., Kasai K., Takatsu H., Shin H.-W., Nakayama K.;
RT "Identification and characterization of novel isoforms of COP I
RT subunits.";
RL J. Biochem. 128:793-801(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=20272150; PubMed=10810093; DOI=10.1101/gr.10.5.703;
RA Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
RT "Identification of novel human genes evolutionarily conserved in
RT Caenorhabditis elegans by comparative proteomics.";
RL Genome Res. 10:703-713(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC TISSUE=Umbilical cord blood;
 RX MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
 RT "Cloning and functional analysis of cDNAs with open reading frames for
 RT 300 previously undefined genes expressed in CD34+ hematopoietic
 RT stem/progenitor cells.";
 RL Genome Res. 10:1546-1560(2000).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RA Tu Q., Yu L., Hu P.R., Zhang H.L., Huang J., Zhao S.Y.;
 RT "Cloning and expression of a new human cDNA homology to B.taurus z-cop
 RT mRNA.";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Mural R.J., Istrail S., Sutton G.G., Florea L., Halpern A.L.,
 RA Mobarry C.M., Lippert R., Walenz B., Shatkay H., Dew I., Miller J.R.,
 RA Flanigan M.J., Edwards N.J., Bolanos R., Fasulo D., Halldorsson B.V.,
 RA Hennenhall S., Turner R., Yooseph S., Lu F., Nusskern D.R.,
 RA Shue B.C., Zheng X.H., Zhong F., Delcher A.L., Huson D.H.,
 RA Kravitz S.A., Mouchard L., Reinert K., Remington K.A., Clark A.G.,
 RA Waterman M.S., Eichler E.E., Adams M.D., Hunkapiller M.W., Myers E.W.,
 RA Venter J.C.;
 RL Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Placenta;
 RX PubMed=15489334; DOI=10.1101/gr.2596504;
 RG The MGC Project Team;
 RT "The status, quality, and expansion of the NIH full-length cDNA
 RT project: the Mammalian Gene Collection (MGC).";
 RL Genome Res. 14:2121-2127(2004).
 RN [7]
 RP PROTEIN SEQUENCE OF 1-14, ACETYLATION AT MET-1, AND MASS SPECTROMETRY.
 RC TISSUE=Colon carcinoma;
 RA Bienvenut W.V., Zebisch A., Kolch W.;
 RL Submitted (DEC-2008) to UniProtKB.
 RN [8]
 RP PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT SER-161, AND MASS
 RP SPECTROMETRY.
 RC TISSUE=Embryonic kidney;
 RX PubMed=17525332; DOI=10.1126/science.1140321;
 RA Matsuoka S., Ballif B.A., Smogorzewska A., McDonald E.R. III,
 RA Hurov K.E., Luo J., Bakalarski C.E., Zhao Z., Solimini N.,
 RA Lerenthal Y., Shiloh Y., Gygi S.P., Elledge S.J.;
 RT "ATM and ATR substrate analysis reveals extensive protein networks
 RT responsive to DNA damage.";
 RL Science 316:1160-1166(2007).
 RN [9]
 RP IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].
 RA Colinge J., Superti-Furga G., Bennett K.L.;
 RL Submitted (OCT-2008) to UniProtKB.
 RN [10]
 RP ACETYLATION [LARGE SCALE ANALYSIS] AT MET-1, AND MASS SPECTROMETRY.
 RC TISSUE=Embryonic kidney;
 RX PubMed=19413330; DOI=10.1021/ac9004309;
 RA Gauci S., Helbig A.O., Slijper M., Krijgsvelde J., Heck A.J.,
 RA Mohammed S.;
 RT "Lys-N and trypsin cover complementary parts of the phosphoproteome in
 RT a refined SCX-based approach.";
 RL Anal. Chem. 81:4493-4501(2009).
 RN [11]
 RP STRUCTURE BY NMR.
 RA Yu W., Jin C., Xia B.;
 RT "The NMR structure of human zeta-COP.";

```

RL Submitted (JUN-2007) to the PDB data bank.
CC
CC -!- FUNCTION: The coatomer is a cytosolic protein complex that binds
CC to dilysine motifs and reversibly associates with Golgi non-
CC clathrin-coated vesicles, which further mediate biosynthetic
CC protein transport from the ER, via the Golgi up to the trans Golgi
CC network. Coatomer complex is required for budding from Golgi
CC membranes, and is essential for the retrograde Golgi-to-ER
CC transport of dilysine-tagged proteins. In mammals, the coatomer
CC can only be recruited by membranes associated to ADP-ribosylation
CC factors (ARFs), which are small GTP-binding proteins; the complex
CC also influences the Golgi structural integrity, as well as the
CC processing, activity, and endocytic recycling of LDL receptors (By
CC similarity).
CC
CC -!- FUNCTION: The zeta subunit may be involved in regulating the coat
CC assembly and, hence, the rate of biosynthetic protein transport
CC due to its association-dissociation properties with the coatomer
CC complex.
CC
CC -!- SUBUNIT: Oligomeric complex that consists of at least the alpha,
CC beta, beta', gamma, delta, epsilon and zeta subunits.
CC
CC -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity). Golgi apparatus
CC membrane; Peripheral membrane protein; Cytoplasmic side (By
CC similarity). Cytoplasmic vesicle, COPI-coated vesicle membrane;
CC Peripheral membrane protein; Cytoplasmic side (By similarity).
CC Note=The coatomer is cytoplasmic or polymerized on the cytoplasmic
CC side of the Golgi, as well as on the vesicles/buds originating
CC from it (By similarity).
CC
CC -!- PTM: Phosphorylated upon DNA damage, probably by ATM or ATR.
CC
CC -!- SIMILARITY: Belongs to the adaptor complexes small subunit family.
CC
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB047848; BAB17659.1; -; mRNA.
DR EMBL; AF151878; AAD34115.1; -; mRNA.
DR EMBL; AF161529; AAF29144.1; -; mRNA.
DR EMBL; AF086911; AAP97141.1; -; mRNA.
DR EMBL; CH471054; EAW96774.1; -; Genomic_DNA.
DR EMBL; BC002849; AAH02849.1; -; mRNA.
DR IPI; IPI00032851; -.
DR RefSeq; NP_057141.1; -.
DR UniGene; Hs.505652; -.
DR PDB; 2HF6; NMR; -; A=1-149.
DR PDBsum; 2HF6; -.
DR ProteinModelPortal; P61923; -.
DR DIP; DIP-29873N; -.
DR IntAct; P61923; 3.
DR STRING; P61923; -.
DR PhosphoSite; P61923; -.
DR PRIDE; P61923; -.
DR Ensembl; ENST00000262061; ENSP00000262061; ENSG00000111481.
DR GeneID; 22818; -.
DR KEGG; hsa:22818; -.
DR UCSC; uc001sfs.1; human.
DR CTD; 22818; -.
DR GeneCards; GC12P054718; -.
DR H-InvDB; HIX0010694; -.
DR HGNC; HGNC:2243; COP21.
DR PharmGKB; PA26760; -.
DR eggNOG; prNOG08087; -.
DR HOGENOM; HBG326766; -.
DR HOVERGEN; HBG051077; -.
DR InParanoid; P61923; -.
DR OMA; YDDTYPT; -.
DR PhylomeDB; P61923; -.
DR Reactome; REACT_11123; Membrane Trafficking.
DR NextBio; 43208; -.
DR ArrayExpress; P61923; -.

```

DR Bgee; P61923; -.
 DR CleanEx; HS_COP21; -.
 DR Genevestigator; P61923; -.
 DR GermOnline; ENSG00000111481; Homo sapiens.
 DR GO; GO:0030126; C:COPI vesicle coat; IDA:UniProtKB.
 DR GO; GO:0005829; C:cytosol; EXP:Reactome.
 DR GO; GO:0005515; F:protein binding; IEA:InterPro.
 DR GO; GO:0048205; P:COPI coating of Golgi vesicle; EXP:Reactome.
 DR GO; GO:0006891; P:intra-Golgi vesicle-mediated transport; IDA:UniProtKB.
 DR GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
 DR GO; GO:0006890; P:retrograde vesicle-mediated transport, Golg. . . ; TAS:UniProtKB.
 DR InterPro; IPR022775; AP_mu_sigma_su.
 DR InterPro; IPR000804; Clathrin_sm-chain_CS.
 DR InterPro; IPR011012; Longin-like.
 DR Pfam; PF01217; Clat_adaptor_s; 1.
 DR SUPFAM; SSF64356; Longin_like; 1.
 DR PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
 PE 1: Evidence at protein level;
 KW 3D-structure; Acetylation; Complete proteome; Cytoplasm;
 KW Cytoplasmic vesicle; Direct protein sequencing; ER-Golgi transport;
 KW Golgi apparatus; Membrane; Phosphoprotein; Protein transport;
 KW Transport.
 FT CHAIN 1 177 Coatomer subunit zeta-1.
 FT /FTId=PRO_0000193825.
 FT MOD_RES 1 1 N-acetylmethionine.
 FT MOD_RES 161 161 Phosphoserine.
 FT STRAND 14 20
 FT STRAND 25 30
 FT HELIX 38 52
 FT STRAND 59 62
 FT STRAND 65 72
 FT STRAND 75 81
 FT HELIX 88 105
 FT HELIX 111 115
 FT HELIX 118 128
 FT HELIX 139 148

Query Match 100.0%; Score 882; DB 1; Length 177;
 Best Local Similarity 100.0%;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEALILEPSLYTVKAILILDNDGDRLEFAKYDDTYPVKEQKAFKFNIFNKTHTRDSEIA 60
 Db 1 MEALILEPSLYTVKAILILDNDGDRLEFAKYDDTYPVKEQKAFKFNIFNKTHTRDSEIA 60
 Qy 61 LLEGLTVVYKSSIDLIFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLNMEG 120
 Db 61 LLEGLTVVYKSSIDLIFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLNMEG 120
 Qy 121 LFLAVDEIVDGGVILESDPQQVVRVALRGEDVPLTEQTVSQVLQSAKEIKWSLLR 177
 Db 121 LFLAVDEIVDGGVILESDPQQVVRVALRGEDVPLTEQTVSQVLQSAKEIKWSLLR 177

RESULT 2

COP21_MOUSE

ID COP21_MOUSE Reviewed; 177 AA.
 AC P61924; Q9Y3C3;
 DT 07-JUN-2004, integrated into UniProtKB/Swiss-Prot.
 DT 07-JUN-2004, sequence version 1.
 DT 05-OCT-2010, entry version 58.
 DE RecName: Full=Coatomer subunit zeta-1;
 DE AltName: Full=Zeta-1-coat protein;
 DE Short=Zeta-1 COP;
 GN Name=Cop21; Synonyms=Copz;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RA Hahn Y., Chung J.H.;
 RT "Murine Copz1 gene encoding nonclathrin coat protein zeta-COP.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioloni M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Huminicki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasaki Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schoenbach C., Sekiguchi K., Sempke C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmer S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6, and C57BL/6J; TISSUE=Brain, and Embryo;
 RX PubMed=15489334; DOI=10.1101/gr.2596504;
 RG The MGC Project Team;
 RT "The status, quality, and expansion of the NIH full-length cDNA
 project: the Mammalian Gene Collection (MGC).";
 RL Genome Res. 14:2121-2127(2004).
 CC -!- FUNCTION: The coatamer is a cytosolic protein complex that binds
 CC to dilysine motifs and reversibly associates with Golgi non-
 CC clathrin-coated vesicles, which further mediate biosynthetic
 CC protein transport from the ER, via the Golgi up to the trans Golgi
 CC network. Coatamer complex is required for budding from Golgi
 CC membranes, and is essential for the retrograde Golgi-to-ER
 CC transport of dilysine-tagged proteins. In mammals, the coatamer
 CC can only be recruited by membranes associated to ADP-ribosylation

factors (ARFs), which are small GTP-binding proteins; the complex also influences the Golgi structural integrity, as well as the processing, activity, and endocytic recycling of LDL receptors (By similarity).

FUNCTION: The zeta subunit may be involved in regulating the coat assembly and, hence, the rate of biosynthetic protein transport due to its association-dissociation properties with the coatomeer complex (By similarity).

SUBUNIT: Oligomeric complex that consists of at least the alpha, beta, beta', gamma, delta, epsilon and zeta subunits (By similarity).

SUBCELLULAR LOCATION: Cytoplasm (By similarity). Golgi apparatus membrane; Peripheral membrane protein; Cytoplasmic side (By similarity). Cytoplasmic vesicle, COPI-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side (By similarity). Note=The coatomeer is cytoplasmic or polymerized on the cytoplasmic side of the Golgi, as well as on the vesicles/buds originating from it (By similarity).

PTM: Phosphorylated upon DNA damage, probably by ATM or ATR (By similarity).

SIMILARITY: Belongs to the adaptor complexes small subunit family.

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EMBL; AB037370; BAA90303.1; -; mRNA.
EMBL; AK003302; BAB22703.1; -; mRNA.
EMBL; BC002246; -; NOT_ANNOTATED_CDS; mRNA.
EMBL; BC058524; AAH58524.1; -; mRNA.
EMBL; BC085314; AAH85314.1; -; mRNA.
IPI; IPI00139637; -.
RefSeq; NP_062791.1; -.
UniGene; Mm.29473; -.
ProteinModelPortal; P61924; -.
SMR; P61924; 1-149.
STRING; P61924; -.
PhosphoSite; P61924; -.
PRIDE; P61924; -.
Ensembl; ENSMUST00000100162; ENSMUSP00000097738; ENSMUSG00000060992.
GeneID; 56447; -.
KEGG; mmu:56447; -.
UCSC; uc007xxv.1; mouse.
CTD; 56447; -.
MGI; MGI:1929063; Copz1.
eggNOG; roNOG15155; -.
HOGENOM; HBG326766; -.
HOVERGEN; HBG051077; -.
InParanoid; P61924; -.
OMA; YDDTYPT; -.
PhylomeDB; P61924; -.
NextBio; 312654; -.
ArrayExpress; P61924; -.
Bgee; P61924; -.
CleanEx; MM_COP21; -.
Genevestigator; P61924; -.
GermOnline; ENSMUSG00000060992; Mus musculus.
GO; GO:0030126; C:COPI vesicle coat; ISS:UniProtKB.
GO; GO:0005515; F:protein binding; IEA:InterPro.
GO; GO:0006891; P:intra-Golgi vesicle-mediated transport; ISS:UniProtKB.
GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
InterPro; IPR022775; AP_mu_sigma_su.
InterPro; IPR000804; Clathrin_sm-chain_CS.
InterPro; IPR011012; Longin-like.
Pfam; PF01217; Clat_adaptor_s; 1.
SUPFAM; SSF64356; Longin_like; 1.
PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE 2: Evidence at transcript level;

KW Acetylation; Cytoplasm; Cytoplasmic vesicle; ER-Golgi transport;
 KW Golgi apparatus; Membrane; Phosphoprotein; Protein transport;
 KW Transport.
 FT CHAIN 1 177 Coatomer subunit zeta-1.
 FT /FTId=PRO_0000193826.
 FT MOD_RES 1 1 N-acetylmethionine (By similarity).
 FT MOD_RES 161 161 Phosphoserine (By similarity).
 SQ SEQUENCE 177 AA; 20198 MW; 35553D032D3A049 CRC64;

Query Match 100.0%; Score 882; DB 1; Length 177;
 Best Local Similarity 100.0%;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEALILEPSLYTVKAILILDNDGDRFLAKYYDDTYPVKEQKAFKFNKTHRTDSEIA 60
 Db 1 MEALILEPSLYTVKAILILDNDGDRFLAKYYDDTYPVKEQKAFKFNKTHRTDSEIA 60
 Qy 61 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
 Db 61 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
 Qy 121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEIKWSLLR 177
 Db 121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEIKWSLLR 177

RESULT 3

COPZ1_PONAB

ID COPZ1_PONAB Reviewed; 177 AA.
 AC Q5R5F2;
 DT 13-SEP-2005, integrated into UniProtKB/Swiss-Prot.
 DT 21-DEC-2004, sequence version 1.
 DT 05-OCT-2010, entry version 37.
 DE RecName: Full=Coatomer subunit zeta-1;
 DE AltName: Full=Zeta-1-coat protein;
 DE Short=Zeta-1 COP;
 GN Name=COPZ1; Synonyms=COPZ;
 OS Pongo abelii (Sumatran orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Pongo.
 OX NCBI_TaxID=9601;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Kidney;
 RG The German cDNA consortium;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: The coatomer is a cytosolic protein complex that binds
 CC to dilysine motifs and reversibly associates with Golgi non-
 CC clathrin-coated vesicles, which further mediate biosynthetic
 CC protein transport from the ER, via the Golgi up to the trans Golgi
 CC network. Coatomer complex is required for budding from Golgi
 CC membranes, and is essential for the retrograde Golgi-to-ER
 CC transport of dilysine-tagged proteins. In mammals, the coatomer
 CC can only be recruited by membranes associated to ADP-ribosylation
 CC factors (ARFs), which are small GTP-binding proteins; the complex
 CC also influences the Golgi structural integrity, as well as the
 CC processing, activity, and endocytic recycling of LDL receptors (By
 CC similarity).
 CC -!- FUNCTION: The zeta subunit may be involved in regulating the coat
 CC assembly and, hence, the rate of biosynthetic protein transport
 CC due to its association-dissociation properties with the coatomer
 CC complex (By similarity).
 CC -!- SUBUNIT: Oligomeric complex that consists of at least the alpha,
 CC beta, beta', gamma, delta, epsilon and zeta subunits (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity). Golgi apparatus

CC membrane; Peripheral membrane protein; Cytoplasmic side (By
 CC similarity). Cytoplasmic vesicle, COPI-coated vesicle membrane;
 CC Peripheral membrane protein; Cytoplasmic side (By similarity).
 CC Note=The coatomer is cytoplasmic or polymerized on the cytoplasmic
 CC side of the Golgi, as well as on the vesicles/buds originating
 CC from it (By similarity).
 CC -!- PTM: Phosphorylated upon DNA damage, probably by ATM or ATR (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the adaptor complexes small subunit family.
 CC -----
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 CC -----
 DR EMBL; CR860909; CAH93014.1; -. mRNA.
 DR RefSeq; NP_001127620.1; -.
 DR UniGene; Pab.18608; -.
 DR ProteinModelPortal; Q5R5F2; -.
 DR SMR; Q5R5F2; 1-149.
 DR GeneID; 100174699; -.
 DR CTD; 100174699; -.
 DR HOVERGEN; HBG051077; -.
 DR InParanoid; Q5R5F2; -.
 DR OMA; YDDTYPT; -.
 DR OrthoDB; EOG969TD6; -.
 DR GO; GO:0030126; C:COPI vesicle coat; ISS:UniProtKB.
 DR GO; GO:0005515; F:protein binding; IEA:InterPro.
 DR GO; GO:0006891; P:intra-Golgi vesicle-mediated transport; ISS:UniProtKB.
 DR GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
 DR InterPro; IPR022775; AP_mu_sigma_su.
 DR InterPro; IPR000804; Clathrin-sm-chain_CS.
 DR InterPro; IPR011012; Longin-like.
 DR Pfam; PF01217; Clat_adaptor_s; 1.
 DR SUPFAM; SSF64356; Longin_like; 1.
 DR PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
 PE 2: Evidence at transcript level;
 KW Acetylation; Cytoplasm; Cytoplasmic vesicle; ER-Golgi transport;
 KW Golgi apparatus; Membrane; Phosphoprotein; Protein transport;
 KW Transport.
 FT CHAIN 1 177 Coatomer subunit zeta-1.
 FT /FTId=PRO_0000193827.
 FT MOD_RES 1 1 N-acetylmethionine (By similarity).
 FT MOD_RES 161 161 Phosphoserine (By similarity).
 SQ SEQUENCE 177 AA; 20198 MW; 35553D032D3A049 CRC64;

Query Match 100.0%; Score 882; DB 1; Length 177;
 Best Local Similarity 100.0%;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPSVKEQKAFKFNKTHRTDSEIA	60
Db	1	MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPSVKEQKAFKFNKTHRTDSEIA	60
Qy	61	LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLNMEG	120
Db	61	LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLNMEG	120
Qy	121	LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEIKWSLLR	177
Db	121	LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEIKWSLLR	177

RESULT 4
 D4A8T3_RAT
 ID D4A8T3_RAT Unreviewed; 177 AA.
 AC D4A8T3;
 DT 20-APR-2010, integrated into UniProtKB/TrEMBL.
 DT 20-APR-2010, sequence version 1.

DT 02-NOV-2010, entry version 7.
 DE SubName: Full=Coatomer protein complex, subunit zeta 1 (Predicted);
 DE SubName: Full=Uncharacterized protein;
 GN Name=Copz1; Synonyms=Copz1_predicted; ORFNames=rCG_50578;
 OS *Rattus norvegicus* (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP IDENTIFICATION.
 RG Ensembl;
 RL Submitted (MAR-2010) to UniProtKB.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Brown Norway;
 RX PubMed=15057822; DOI=10.1038/nature02426;
 RA Gibbs R.A., Weinstock G.M., Metzker M.L., Muzny D.M., Sodergren E.J.,
 RA Scherer S., Scott G., Steffen D., Worley K.C., Burch P.E., Okunou G.,
 RA Hines S., Lewis L., Deramo C., Delgado O., Dugan-Rocha S., Miner G.,
 RA Morgan M., Hawes A., Gill R., Holt R.A., Adams M.D., Amanatides P.G.,
 RA Baden-Tillson H., Barnstead M., Chin S., Evans C.A., Ferriera S.,
 RA Foster C., Glodek A., Gu Z., Jennings D., Kraft C.L., Nguyen T.,
 RA Pfannkuch C.M., Sitter C., Sutton G.G., Venter J.C., Woodage T.,
 RA Smith D., Lee H.-M., Gustafson E., Cahill P., Kana A.,
 RA Doucette-Stamm L., Weinstock K., Fechtel K., Weiss R.B., Dunn D.M.,
 RA Green E.D., Blakesley R.W., Bouffard G.G., De Jong P.J., Osoegawa K.,
 RA Zhu B., Marra M., Schein J., Bosdet I., Fjell C., Jones S.,
 RA Krzywinski M., Mathewson C., Siddiqui A., Wye N., McPherson J.,
 RA Zhao S., Fraser C.M., Shetty J., Shatsman S., Geer K., Chen Y.,
 RA Abramson S., Nierman W.C., Havlak P.H., Chen R., Durbin K.J., Egan A.,
 RA Ren Y., Song X.-Z., Li B., Liu Y., Qin X., Cawley S., Cooney A.J.,
 RA D'Souza L.M., Martin K., Wu J.Q., Gonzalez-Garay M.L., Jackson A.R.,
 RA Kalafus K.J., McLeod M.P., Milosavljevic A., Virk D., Volkov A.,
 RA Wheeler D.A., Zhang Z., Bailey J.A., Eichler E.E., Tuzun E.,
 RA Birney E., Mongin E., Ureta-Vidal A., Woodward C., Zdobnov E.,
 RA Bork P., Suyama M., Torrents D., Alexandersson M., Trask B.J.,
 RA Young J.M., Huang H., Wang H., Xing H., Daniels S., Gietzen D.,
 RA Schmidt J., Stevens K., Vitt U., Wingrove J., Camara F., Mar Alba M.,
 RA Abril J.F., Guigo R., Smit A., Dubchak I., Rubin E.M., Couronne O.,
 RA Poliakov A., Huebner N., Ganten D., Goesele C., Hummel O.,
 RA Kreitler T., Lee Y.-A., Monti J., Schulz H., Zimdahl H.,
 RA Himmelbauer H., Lehrach H., Jacob H.J., Bromberg S.,
 RA Gullings-Handley J., Jensen-Seaman M.I., Kwitek A.E., Lazar J.,
 RA Pasko D., Tonellato P.J., Twigger S., Ponting C.P., Duarte J.M.,
 RA Rice S., Goodstadt L., Beaton S.A., Emes R.D., Winter E.E.,
 RA Webber C., Brandt P., Nyakatura G., Adetobi M., Chiaromonte F.,
 RA Elnitski L., Eswara P., Hardison R.C., Hou M., Kolbe D., Makova K.,
 RA Miller W., Nekrutenko A., Riemer C., Schwartz S., Taylor J., Yang S.,
 RA Zhang Y., Lindpaintner K., Andrews T.D., Caccamo M., Clamp M.,
 RA Clarke L., Curwen P., Durbin R.M., Eyas E., Searle S.M., Cooper G.M.,
 RA Batzoglu S., Brudno M., Sidow A., Stone E.A., Payseur B.A.,
 RA Bourque G., Lopez-Otin C., Puente X.S., Chakrabarti K., Chatterji S.,
 RA Dewey C., Pachter L., Bray N., Yap V.B., Caspi A., Tesler G.,
 RA Pevzner P.A., Haussler D., Roskin K.M., Baertsch R., Clawson H.,
 RA Furey T.S., Hinrichs A.S., Karolchik D., Kent W.J., Rosenbloom K.R.,
 RA Trumbower H., Weirauch M., Cooper D.N., Stenson P.D., Ma B., Brent M.,
 RA Arumugam M., Shteynberg D., Copley R.R., Taylor M.S., Riethman H.,
 RA Mudunuri U., Peterson J., Guyer M., Felsenfeld A., Old S., Mockrin S.,
 RA Collins F.S.;
 RT "Genome sequence of the Brown Norway rat yields insights into
 RT mammalian evolution."
 RL Nature 428:493-521(2004).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BN;
 RX PubMed=15632090; DOI=10.1101/gr.2889405;

RA Florea L., Di Francesco V., Miller J., Turner R., Yao A., Harris M.,
 RA Walenz B., Mobarry C., Merkulo G.V., Charlab R., Dew I., Deng Z.,
 RA Istrail S., Li P., Sutton G.;
 RT "Gene and alternative splicing annotation with AIR.";
 RL Genome Res. 15:54-66(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BN;
 RA Mural R.J., Li P.W., Adams M.D., Amanatides P.G., Baden-Tillson H.,
 RA Barnstead M., Chin S.H., Dew I., Evans C.A., Ferriera S., Flanagan M.,
 RA Fosler C., Glodek A., Gu Z., Holt R.A., Jennings D., Kraft C.L.,
 RA Lu F., Nguyen T., Nusskern D.R., Pfannkuch C.M., Sitter C.,
 RA Sutton G.G., Venter J.C., Wang Z., Woodage T., Zheng X.H., Zhong F.;
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.

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 CC -----

DR EMBL; CH474035; EDL86787.1; -; Genomic_DNA.
 DR IPI; IPI00949165; -.
 DR RefSeq; NP_001101587.1; -.
 DR UniGene; Rn.159796; -.
 DR ProteinModelPortal; D4A8T3; -.
 DR SMR; D4A8T3; 1-149.
 DR Ensembl; ENSRN000000065270; ENSRNOP00000059082; ENSRNOG00000036835.
 DR GeneID; 315345; -.
 DR KEGG; rno:315345; -.
 DR CTD; 315345; -.
 DR RGD; 1306154; Copz1.
 DR GO; GO:0030117; C:membrane coat; IEA:InterPro.
 DR GO; GO:0005515; F:protein binding; IEA:InterPro.
 DR GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
 DR GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
 DR InterPro; IPR022775; AP_mu_sigma_su.
 DR InterPro; IPR000804; Clathrin_sm-chain_CS.
 DR InterPro; IPR011012; Longin-like.
 DR Pfam; PF01217; Clat_adaptor_s; 1.
 DR SUPFAM; SSF64356; Longin_like; 1.
 DR PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
 PE 4: Predicted;
 SQ SEQUENCE 177 AA; 20198 MW; 355530D032D3A049 CRC64;

Query Match 100.0%; Score 882; DB 2; Length 177;
 Best Local Similarity 100.0%;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEALILEPSLYTVKAILILDNDGDLFAKYDDTYPVSKQKAFKFNIFNKHRTDSEIA	60
Db	1	MEALILEPSLYTVKAILILDNDGDLFAKYDDTYPVSKQKAFKFNIFNKHRTDSEIA	60
Qy	61	LLEGLTVVYKSSIDLIFYFYIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLNMEG	120
Db	61	LLEGLTVVYKSSIDLIFYFYIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLNMEG	120
Qy	121	LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR	177
Db	121	LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR	177

RESULT 5

Q542M2_MOUSE

ID Q542M2_MOUSE Unreviewed; 177 AA.
 AC Q542M2;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 05-OCT-2010, entry version 50.
 DE SubName: Full=Coatomer protein complex, subunit zeta 1, isoform CRA_c;

DE SubName: Full=Copz1 protein;
 DE SubName: Full=Putative uncharacterized protein;
 GN Name=Copz1; ORFNames=mCG_15682;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J, and NOD; TISSUE=Spinal ganglion, Amnion, Placenta,
 RC and Activated spleen;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Humenick L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasaki Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schoenbach C., Sekiguchi K., Sempere C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusci V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima T., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Mixed;
 RX MEDLINE=22036378; PubMed=12040188; DOI=10.1126/science.1069193;
 RA Mural R.J., Adams M.D., Myers E.W., Smith H.O., Miklos G.L., Wides R.,
 RA Halpern A., Li P.W., Sutton G.G., Nadeau J., Salzberg S.L., Holt R.A.,
 RA Kodira C.D., Lu F., Chen L., Deng Z., Evangelista C.C., Gan W.,
 RA Heiman T.J., Li J., Li Z., Merkulov G.V., Milshina N.V., Naik A.K.,
 RA Qi R., Shue B.C., Wang A., Wang J., Wang X., Yan X., Ye J.,
 RA Yooseph S., Zhao Q., Zheng L., Zhu S.C., Biddick K., Bolanos R.,
 RA Delcher A.L., Dew I.M., Fasulo D., Flanigan M.J., Huseon D.H.,
 RA Kravitz S.A., Miller J.R., Mobarry C.M., Reinert K., Remington K.A.,
 RA Zhang Q., Zheng X.H., Nusskern D.R., Lai Z., Lei Y., Zhong W., Yao A.,
 RA Guan P., Ji R.R., Gu Z., Wang Z.Y., Zhong F., Xiao C., Chiang C.C.,
 RA Yandell M., Wortman J.R., Amanatides P.G., Hladun S.L., Pratts E.C.,

RA Johnson J.E., Dodson K.L., Woodford K.J., Evans C.A., Gropman B.,
RA Rusch D.B., Venter E., Wang M., Smith T.J., Houck J.T., Tompkins D.E.,
RA Haynes C., Jacob D., Chin S.H., Allen D.R., Dahlke C.E., Sanders R.,
RA Li K., Liu X., Levitsky A.A., Majoros W.H., Chen Q., Xia A.C.,
RA Lopez J.R., Donnelly M.T., Newman M.H., Glodek A., Kraft C.L.,
RA Nodell M., Ali F., An H.J., Baldwin-Pitts D., Beeson K.Y., Cai S.,
RA Carnes M., Carver A., Caulk P.M., Center A., Chen Y.H., Cheng M.L.,
RA Coyne M.D., Crowder M., Danaher S., Davenport L.B., Desilets R.,
RA Dietz S.M., Doup L., Dullaghan P., Ferriera S., Fosler C.R.,
RA Gire H.C., Gluecksmann A., Gocayne J.D., Gray J., Hart B., Haynes J.,
RA Hoover J., Howland T., Ibegwam C., Jalali M., Johns D., Kline L.,
RA Ma D.S., MacCawley S., Magoon A., Mann F., May D., McIntosh T.C.,
RA Mehta S., Moy L., Moy M.C., Murphy B.J., Murphy S.D., Nelson K.A.,
RA Nuri Z., Parker K.A., Prudhomme A.C., Puri V.N., Qureshi H.,
RA Raley J.C., Reardon M.S., Regier M.A., Rogers Y.H., Romblad D.L.,
RA Schutz J., Scott J.L., Scott R., Sitter C.D., Smallwood M.,
RA Sprague A.C., Stewart E., Strong R.V., Suh E., Sylvester K.,
RA Thomas R., Tint N.N., Tsonis C., Wang G., Wang G., Williams M.S.,
RA Williams S.M., Windsor S.M., Wolfe K., Wu M.M., Zaveri J.,
RA Chaturvedi K., Gabrielian A.E., Ke Z., Sun J., Subramanian G.,
RA Venter J.C., Pfannkoch C.M., Barnstead M., Stephenson L.D.;
RT "A comparison of whole-genome shotgun-derived mouse chromosome 16 and
RT the human genome.";
RL Science 296:1661-1671(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mixed;
RA Mural R.J., Adams M.D., Myers E.W., Smith H.O., Venter J.C.;
RL Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=Czech II; TISSUE=Mammary tumor metastatized to lung. Tumor
RC arose spontaneously;
RX PubMed=15489334; DOI=10.1101/gr.2596504;
RG The MGC Project Team;
RT "The status, quality, and expansion of the NIH full-length cDNA
RT project: the Mammalian Gene Collection (MGC).";
RL Genome Res. 14:2121-2127(2004).
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CC -----
DR EMBL; BC110679; AAI10680.1; -; mRNA.
DR EMBL; AK083824; BAC39030.1; -; mRNA.
DR EMBL; AK156758; BAE33841.1; -; mRNA.
DR EMBL; AK167636; BAE39687.1; -; mRNA.
DR EMBL; AK168382; BAE40310.1; -; mRNA.
DR EMBL; AK168471; BAE40362.1; -; mRNA.
DR EMBL; CH466550; EDL03927.1; -; Genomic_DNA.
DR IPI; IPI00139637; -.
DR RefSeq; NP_062791.1; -.
DR UniGene; Mm.29473; -.
DR ProteinModelPortal; Q542M2; -.
DR SMR; Q542M2; 1-149.
DR STRING; Q542M2; -.
DR PRIDE; Q542M2; -.
DR Ensembl; ENSMUST00000100162; ENSMUSP00000097738; ENSMUSG00000060992.
DR GeneID; 56447; -.
DR KEGG; mmu:56447; -.
DR CTD; 56447; -.
DR MGI; MGI:1929063; Copz1.
DR HOVERGEN; HBG051077; -.
DR InParanoid; Q542M2; -.
DR OMA; YDDTYPT; -.
DR PhylomeDB; Q542M2; -.
DR NextBio; 312654; -.
DR ArrayExpress; Q542M2; -.

DR Bgee; Q542M2; -.
 DR Genevestigator; Q542M2; -.
 DR GO; GO:0030117; C:membrane coat; IEA:InterPro.
 DR GO; GO:0005515; F:protein binding; IEA:InterPro.
 DR GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
 DR InterPro; IPR022775; AP_mu_sigma_su.
 DR InterPro; IPR000804; Clathrin-sm-chain_CS.
 DR InterPro; IPR011012; Longin-like.
 DR Pfam; PF01217; Clat_adaptor_s; 1.
 DR SUPFAM; SSF64356; Longin_like; 1.
 DR PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
 PE 2: Evidence at transcript level;
 SQ SEQUENCE 177 AA; 20198 MW; 355530D032D3A049 CRC64;

Query Match 100.0%; Score 882; DB 2; Length 177;
 Best Local Similarity 100.0%;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEALILEPSLYTVKAILILDNDGDLFAKYDDTYPVSKQKAFKFNIFNKHRTDSEIA 60
 Db 1 MEALILEPSLYTVKAILILDNDGDLFAKYDDTYPVSKQKAFKFNIFNKHRTDSEIA 60

Qy 61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLNMEG 120
 Db 61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLNMEG 120

Qy 121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
 Db 121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177

RESULT 6

COPZ1_BOVIN
 ID COPZ1_BOVIN Reviewed; 177 AA.
 AC P35604; Q5EA44;
 DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
 DT 27-JUN-2006, sequence version 2.
 DT 05-OCT-2010, entry version 74.
 DE RecName: Full=Coatomer subunit zeta-1;
 DE AltName: Full=Zeta-1-coat protein;
 DE Short=Zeta-1 COP;
 GN Name=COPZ1; Synonyms=COPZ;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND PROTEIN SEQUENCE OF 55-70; 113-129 AND
 RP 146-160.
 RC TISSUE=Liver;
 RX MEDLINE=94103328; PubMed=8276893; DOI=10.1083/jcb.123.6.1727;
 RA Kuge O., Hara-Kuge S., Orci L., Ravazzola M., Amherdt M., Tanigawa G.,
 RA Wieland F.T., Rothman J.E.;
 RT "Zeta-COP, a subunit of coatomer, is required for COP-coated vesicle
 RT assembly.";
 RL J. Cell Biol. 123:1727-1734(1993).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX PubMed=16305752; DOI=10.1186/1471-2164-6-166;
 RA Harhay G.P., Sonstegard T.S., Keele J.W., Heaton M.P., Clawson M.L.,
 RA Snelling W.M., Wiedmann R.T., Van Tassell C.P., Smith T.P.L.;
 RT "Characterization of 954 bovine full-CDS cDNA sequences.";
 RL BMC Genomics 6:166-166(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=Crossbred X Angus; TISSUE=Ileum;

```

RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC
CC -!- FUNCTION: The coatamer is a cytosolic protein complex that binds
CC to dilysine motifs and reversibly associates with Golgi non-
CC clathrin-coated vesicles, which further mediate biosynthetic
CC protein transport from the ER, via the Golgi up to the trans Golgi
CC network. Coatamer complex is required for budding from Golgi
CC membranes, and is essential for the retrograde Golgi-to-ER
CC transport of dilysine-tagged proteins. In mammals, the coatamer
CC can only be recruited by membranes associated to ADP-ribosylation
CC factors (ARFs), which are small GTP-binding proteins; the complex
CC also influences the Golgi structural integrity, as well as the
CC processing, activity, and endocytic recycling of LDL receptors (By
CC similarity).
CC
CC -!- FUNCTION: The zeta subunit may be involved in regulating the coat
CC assembly and, hence, the rate of biosynthetic protein transport
CC due to its association-dissociation properties with the coatamer
CC complex.
CC
CC -!- SUBUNIT: Oligomeric complex that consists of at least the alpha,
CC beta, beta', gamma, delta, epsilon and zeta subunits.
CC
CC -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity). Golgi apparatus
CC membrane; Peripheral membrane protein; Cytoplasmic side (By
CC similarity). Cytoplasmic vesicle, COPI-coated vesicle membrane;
CC Peripheral membrane protein; Cytoplasmic side (By similarity).
CC Note=The coatamer is cytoplasmic or polymerized on the cytoplasmic
CC side of the Golgi, as well as on the vesicles/buds originating
CC from it (By similarity).
CC
CC -!- PTM: Phosphorylated upon DNA damage, probably by ATM or ATR (By
CC similarity).
CC
CC -!- SIMILARITY: Belongs to the adaptor complexes small subunit family.
CC
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CC -----
DR EMBL; X75935; CAA53539.1; -; mRNA.
DR EMBL; BT020662; AAX08679.1; -; mRNA.
DR EMBL; BT020725; AAX08742.1; -; mRNA.
DR EMBL; BC102358; AAI02359.1; -; mRNA.
DR IPI; IPI00685319; -.
DR PIR; A49465; A49465.
DR RefSeq; NP_776707.2; -.
DR UniGene; Bt.43744; -.
DR ProteinModelPortal; P35604; -.
DR SMR; P35604; 1-149.
DR IntAct; P35604; 2.
DR STRING; P35604; -.
DR Ensembl; ENSBTAT00000007088; ENSBTAP00000007088; ENSBTAG00000005384.
DR GeneID; 281707; -.
DR KEGG; bta:281707; -.
DR CTD; 281707; -.
DR eggNOG; maNOG17869; -.
DR HOVERGEN; HBG051077; -.
DR InParanoid; P35604; -.
DR OMA; YDDTYPT; -.
DR OrthoDB; EOG969TD6; -.
DR PhylomeDB; P35604; -.
DR BioCyc; CATTLE:281707-MONOMER; -.
DR GO; GO:0030126; C:COPI vesicle coat; IDA:UniProtKB.
DR GO; GO:005515; F:protein binding; IEA:InterPro.
DR GO; GO:0006891; P:intra-Golgi vesicle-mediated transport; IDA:UniProtKB.
DR GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR GO; GO:0006890; P:retrograde vesicle-mediated transport, Golg. . . ; TAS:UniProtKB.
DR InterPro; IPR022775; AP_mu_sigma_su.
DR InterPro; IPR000804; Clathrin_sm-chain_CS.
DR InterPro; IPR011012; Longin-like.
DR Pfam; PF01217; Clat_adaptor_s; 1.
DR SUPFAM; SSF64356; Longin_like; 1.

```

DR PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
 PE 1: Evidence at protein level;
 KW Acetylation; Cytoplasm; Cytoplasmic vesicle;
 KW Direct protein sequencing; ER-Golgi transport; Golgi apparatus;
 KW Membrane; Phosphoprotein; Protein transport; Transport.
 FT CHAIN 1 177 Coatomer subunit zeta-1.
 FT /FTid=PRO_0000193824.
 FT MOD_RES 1 1 N-acetylmethionine (By similarity).
 FT MOD_RES 161 161 Phosphoserine (By similarity).
 FT CONFLICT 7 7 E -> Q (in Ref. 1; CAA53539).
 SQ SEQUENCE 177 AA; 20228 MW; D410249532C8BAF8 CRC64;

Query Match 99.5%; Score 878; DB 1; Length 177;
 Best Local Similarity 99.4%;
 Matches 176; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEALILEPSLYTVKAILILDNDGDRLFACYDDTYPVKEQKAFKFNIFNKTHTDSEIA 60
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 Db 1 MEALILEPSLYTVKAILILDNDGDRLFACYDDTYPVKEQKAFKFNIFNKTHTDSEIA 60
 Qy 61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLNMEG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMTVLNCLFDSLSQMLRKNVEKRALLNMEG 120
 Qy 121 LFLAVDEIVDGGVILESDPQQVVRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 LFLAVDEIVDGGVILESDPQQVVRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177

RESULT 7

Q53FU3_HUMAN

ID Q53FU3_HUMAN Unreviewed; 177 AA.
 AC Q53FU3;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 05-OCT-2010, entry version 31.
 DE SubName: Full=Coatomer protein complex, subunit zeta 1 variant;
 DE Flags: Fragment;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Renal proximal tubule;
 RX MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
 RA Maruyama K., Sugano S.;
 RT "Oligo-capping: a simple method to replace the cap structure of
 RT eukaryotic mRNAs with oligoribonucleotides."
 RL Gene 138:171-174(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Renal proximal tubule;
 RX MEDLINE=98038986; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
 RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
 RT "Construction and characterization of a full length-enriched and a 5'-
 RT end-enriched cDNA library."
 RL Gene 200:149-156(1997).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Renal proximal tubule;
 RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
 RA Tanaka A., Yokoyama S.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
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 DR EMBL; AK223188; BAD96908.1; -; mRNA.
 DR IPI; IPI00032851; -.
 DR UniGene; Hs.505652; -.
 DR STRING; Q53FU3; -.
 DR Ensembl; ENST00000262061; ENSP00000262061; ENSG00000111481.
 DR HGNC; HGNC:2243; COP21.
 DR HOVERGEN; HBG051077; -.
 DR ArrayExpress; Q53FU3; -.
 DR Bgee; Q53FU3; -.
 DR GO; GO:0030117; C:membrane coat; IEA:InterPro.
 DR GO; GO:0005515; F:protein binding; IEA:InterPro.
 DR GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
 DR GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
 DR InterPro; IPR022775; AP_mu_sigma_su.
 DR InterPro; IPR00804; Clathrin_sm-chain_CS.
 DR InterPro; IPR011012; Longin-like.
 DR Pfam; PF01217; Clat_adaptor_s; 1.
 DR SUPFAM; SSF64356; Longin_like; 1.
 DR PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
 PE 2: Evidence at transcript level;
 FT NON_TER 1 1
 SQ SEQUENCE 177 AA; 20267 MW; 5E2530D17696A10D CRC64;

Query Match 99.4%; Score 877; DB 2; Length 177;
 Best Local Similarity 99.4%;
 Matches 176; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEALILEPSLYTVKAILILDNDGDRLEFAKYDDTYPVSKQKAFKFNKTHRTDSEIA 60
 Db 1 MEALILEPSLYTVKAILILDNDGDRLEFAKYDDTYPVSKQKAFKFNKTHRTDSEIA 60
 Qy 61 LLEGLTVVYKSSIDLFFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
 Db 61 LLEGLTVVYKSSIDLFFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
 Qy 121 LFLAVDEIVDGGVILESDPQQVVRVALRGEDVPLTEQTVSQVLQSAKEIKWSLLR 177
 Db 121 LFLAVDEIVDGGVILESDPQQVVRVALRGEDVPLTEQTVSQVLQSAKEIKWSLLR 177

RESULT 8

Q28HL1_XENTR
 ID Q28HL1_XENTR Unreviewed; 177 AA.
 AC Q28HL1;
 DT 04-APR-2006, integrated into UniProtKB/TrEMBL.
 DT 04-APR-2006, sequence version 1.
 DT 05-OCT-2010, entry version 22.
 DE SubName: Full=OTTKETP00000008162;
 GN Name=cop2l; ORFNames=TTpA002p21.1-001;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus; Silurana.
 OX NCBI_TaxID=8364;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Amaya E., Ashurst J.L., Bonfield J.K., Croning M.D.R., Chen C-K.,
 RA Davies R.M., Francis M.D., Garrett N., Gilchrist M.J., Grafham D.V.,
 RA McLaren S.R., Papalopulu N., Rogers J., Smith J.C., Taylor R.G.,
 RA Voigt J., Zorn A.M.;
 RL Submitted (OCT-2006) to the EMBL/GenBank/DBJ databases.
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DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR000804; Clathrin_sm-chain_CS.
DR   InterPro; IPR011012; Longin-like.
DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
DR   PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE   2: Evidence at transcript level;
SQ   SEQUENCE   177 AA;  20279 MW;  EC44BED1889FEA07 CRC64;

Query Match          95.8%;  Score 845;  DB 2;  Length 177;
Best Local Similarity 93.2%;
Matches 165;  Conservative 11;  Mismatches 1;  Indels 0;  Gaps 0;

Qy      1  MEALILEPSLYTVKAILILDNDGDLFAKYDDTYPSVKEQKAFKFNKTHRTDSEIA 60
Db      1  MDTLILEPSLYTVKAVLIMDNDGERLYAKYDDTYPTVKEQKAFKFNKTHRTDSEIA 60

Qy     61  LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVKEKRALLENMEG 120
Db     61  LLEGLTVVYKSNIDLYFYFVIGSSHENELMLMSVLNCLFDSLQMLRKNVKEKRALLENMEG 120

Qy    121  LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVS QVLQSAKEIKWSLLR 177
Db    121  LFLAVDEIVDGGVILESDPQQVVHRVALRGDDVPLTEQTVT QVLQSAKEIKWSLLR 177

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RESULT 12

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Q6GGQ0_XENLA
ID   Q6GGQ0_XENLA                      Unreviewed;          177 AA.
AC   Q6GGQ0;
DT   19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2004, sequence version 1.
DT   05-OCT-2010, entry version 33.
DE   SubName: Full=MGC80093 protein;
OS   Name=copz1; Synonyms=MGC80093;
GS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Spleen;
RG   NIH - Xenopus Gene Collection (XGC) project;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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CC   -----
DR   EMBL; BC072784; AAH72784.1; -, mRNA.
DR   RefSeq; NP_001085450.1; -.
DR   UniGene; XL45820; -.
DR   ProteinModelPortal; Q6GGQ0; -.
DR   SMR; Q6GGQ0; 1-149.
DR   GeneID; 443876; -.
DR   KEGG; xla:443876; -.
DR   Xenbase; XB-GENE-6251726; copz1.
DR   HOVERGEN; HBG051077; -.
DR   GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR   GO; GO:0005515; F:protein binding; IEA:InterPro.
DR   GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR   GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR000804; Clathrin_sm-chain_CS.
DR   InterPro; IPR011012; Longin-like.
DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.

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DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
DR   PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE   2: Evidence at transcript level;
SQ   SEQUENCE   177 AA;  20311 MW;  BC44BEC188939BDC CRC64;

Query Match      95.5%;  Score 842;  DB 2;  Length 177;
Best Local Similarity 92.7%;
Matches 164;  Conservative 12;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy    121  LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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RESULT 14

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C3KJY4_ANOFI
ID   C3KJY4_ANOFI                      Unreviewed;          177 AA.
AC   C3KJY4;
DT   16-JUN-2009, integrated into UniProtKB/TrEMBL.
DT   16-JUN-2009, sequence version 1.
DT   05-OCT-2010, entry version 8.
DE   SubName: Full=Coatomer subunit zeta-1;
GN   Name=COP21;
OS   Anoplopoma fimbria (Sablefish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC   Anoplopomatoidei; Anoplopomatidae; Anoplopoma.
OX   NCBI_TaxID=229290;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RA   Messmer A., Rondeau E., Sanderson D., Cooper G., Leong J., Koop B.F.;
RT   "Anoplopoma fimbria ESTs and full-length cDNAs.";
RL   Submitted (MAY-2009) to the EMBL/GenBank/DBJ databases.
CC   -----
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----
DR   EMBL; BT083249; ACQ58956.1; -; mRNA.
DR   GO; GO:0006810; P:transport; IEA:InterPro.
DR   InterPro; IPR022775; AP_mu_sigma_su.
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DR   SUPFAM; SSF64356; Longin_like; 1.
PE   2: Evidence at transcript level;
SQ   SEQUENCE   177 AA;  20187 MW;  E665075A8B25F591 CRC64;

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Query Match      94.8%;  Score 836;  DB 2;  Length 177;
Best Local Similarity 92.7%;
Matches 164;  Conservative 12;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy     61  LLEGLTVVYKSSIDLIFYFVIGSSYENELMLMAVLNCLFDSLSQLMRKNVEKRALLENMEG 120
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DR GO; GO:0005515; F:protein binding; IEA:InterPro.
 DR GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
 DR GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
 DR InterPro; IPR022775; AP_mu_sigma_su.
 DR InterPro; IPR00804; Clathrin_sm-chain_CS.
 DR InterPro; IPR011012; Longin-like.
 DR Pfam; PF01217; Clat_adaptor_s; 1.
 DR SUPFAM; SSF64356; Longin_like; 1.
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 PE 2: Evidence at transcript level;
 SQ SEQUENCE 177 AA; 20273 MW; 2BBAC0388F6E8E69 CRC64;

Query Match 94.3%; Score 832; DB 2; Length 177;
 Best Local Similarity 92.1%;
 Matches 163; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

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Db     61 LLEGLTVVYKSNIDLIFYFVIGSSHENELMLMSVLNCLFDSLSQLRKNVERRALLENMEG 120

Qy    121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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Search completed: December 14, 2010, 11:27:05
 Job time : 96.872 secs

SCORE 36

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103256_us-09-556-178- 5.rapbm.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103256_us-09-556-178-5.rapbm.

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GenCore version 6.3
Copyright (c) 1993 - 2010 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: December 14, 2010, 11:27:17 ; Search time 143 Seconds
(without alignments)
1680.685 Million cell updates/sec

Title: US-09-556-178-5
Perfect score: 882
Sequence: 1 MEALILEPSLYTVKAILILD.....QTVSQVLQSAKEQIKWSLLR 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6210261 seqs, 1354514112 residues

Total number of hits satisfying chosen parameters: 6210261

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*

- 1: /ABSS/Data/CRF/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /ABSS/Data/CRF/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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- 8: /ABSS/Data/CRF/ptodata/1/pubpaa/US12_PUBCOMB.pep:*

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	882	100.0	177	5	US-10-528-183-26	Sequence 26, Appl
2	882	100.0	177	6	US-11-371-354-73107	Sequence 73107, A
3	882	100.0	177	6	US-11-443-428A-819809	Sequence 819809,
4	882	100.0	177	7	US-11-597-825-1351	Sequence 1351, Ap
5	882	100.0	177	8	US-12-399-906-29	Sequence 29, Appl
6	882	100.0	192	6	US-11-443-428A-819804	Sequence 819804,
7	882	100.0	192	6	US-11-443-428A-819805	Sequence 819805,
8	882	100.0	192	6	US-11-443-428A-819806	Sequence 819806,
9	882	100.0	192	6	US-11-443-428A-819808	Sequence 819808,

10	882	100.0	192	6	US-11-443-428A-819810	Sequence 819810,
11	882	100.0	192	6	US-11-443-428A-819816	Sequence 819816,
12	882	100.0	192	6	US-11-443-428A-819818	Sequence 819818,
13	882	100.0	192	6	US-11-443-428A-819819	Sequence 819819,
14	882	100.0	192	6	US-11-443-428A-819821	Sequence 819821,
15	882	100.0	192	6	US-11-443-428A-819823	Sequence 819823,
16	882	100.0	192	6	US-11-443-428A-819825	Sequence 819825,
17	882	100.0	200	6	US-11-443-428A-819807	Sequence 819807,
18	882	100.0	205	6	US-11-443-428A-819812	Sequence 819812,
19	868	98.4	182	6	US-11-443-428A-819814	Sequence 819814,
20	858	97.3	172	6	US-11-443-428A-819813	Sequence 819813,
21	856	97.1	177	6	US-11-443-428A-819815	Sequence 819815,
22	856	97.1	178	6	US-11-443-428A-819811	Sequence 819811,
23	845	95.8	177	4	US-10-403-571-30	Sequence 30, Appl
24	712	80.7	144	4	US-10-425-115-275189	Sequence 275189,
25	712	80.7	144	5	US-10-425-115-275189	Sequence 275189,
26	701	79.5	173	6	US-11-443-428A-819820	Sequence 819820,
27	673	76.3	210	5	US-10-528-183-14	Sequence 14, Appl
28	673	76.3	210	5	US-10-743-643-2465	Sequence 2465, Ap
29	673	76.3	210	6	US-11-371-354-59225	Sequence 59225, A
30	673	76.3	210	8	US-12-399-906-30	Sequence 30, Appl
31	673	76.3	214	6	US-11-443-428A-823399	Sequence 823399,
32	564.5	64.0	160	6	US-11-097-143-7677	Sequence 7677, Ap
33	542	61.5	134	6	US-11-443-428A-819826	Sequence 819826,
34	518	58.7	136	6	US-11-443-428A-823401	Sequence 823401,
35	510	57.8	169	6	US-11-443-428A-823406	Sequence 823406,
36	507.5	57.5	181	7	US-11-360-355-120385	Sequence 120385,
37	507.5	57.5	181	7	US-11-360-355-122102	Sequence 122102,
38	507.5	57.5	181	8	US-12-101-830-120385	Sequence 120385,
39	507.5	57.5	181	8	US-12-101-830-122102	Sequence 122102,
40	487	55.2	177	6	US-11-443-428A-819824	Sequence 819824,
41	454	51.5	138	6	US-11-443-428A-823403	Sequence 823403,
42	441.5	50.1	154	7	US-11-360-355-123790	Sequence 123790,
43	441.5	50.1	154	8	US-12-101-830-123790	Sequence 123790,
44	440	49.9	99	3	US-09-925-297-776	Sequence 776, App
45	440	49.9	125	6	US-11-443-428A-819817	Sequence 819817,

ALIGNMENTS

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RESULT 1
US-10-528-183-26
; Sequence 26, Application US/10528183
; Publication No. US20050226879A1
; GENERAL INFORMATION:
; APPLICANT: Ullman, Katharine
; APPLICANT: Liu, Jin
; APPLICANT: Prunuske, Amy
; APPLICANT: Dimaano, Christian
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATED TO
; TITLE OF INVENTION: INHIBITING NUCLEAR ENVELOPE BREAKDOWN
; FILE REFERENCE: 21101.0045U2
; CURRENT APPLICATION NUMBER: US/10/528,183
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: PCT/US03/29267
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: 60/411,248
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =

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Db 121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177

RESULT 3

US-11-443-428A-819809
 ; Sequence 819809, Application US/11443428A
 ; Publication No. US20070083334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mintz, Liat
 ; APPLICANT: Xie, Hanqing
 ; APPLICANT: Dahari, Dvir
 ; APPLICANT: Levanon, Erez
 ; APPLICANT: Freilich, Shiri
 ; APPLICANT: Beck, Nili
 ; APPLICANT: Zhu, Wei-Yong
 ; APPLICANT: Wasserman, Alon
 ; APPLICANT: Hermesh, Chen
 ; APPLICANT: Azar, Idit
 ; APPLICANT: Bernstein, Jeanne
 ; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
 ; FILE REFERENCE: 02/23929
 ; CURRENT APPLICATION NUMBER: US/11/443,428A
 ; CURRENT FILING DATE: 2006-05-31
 ; NUMBER OF SEQ ID NOS: 1034312
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 819809
 ; LENGTH: 177
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-443-428A-819809

Query Match 100.0%; Score 882; DB 6; Length 177;
 Best Local Similarity 100.0%;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Qy 61 LLEGLTVVYKSSIDLIFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENM 120
 Db 61 LLEGLTVVYKSSIDLIFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENM 120
 Qy 121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
 Db 121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177

RESULT 4

US-11-597-825-1351
 ; Sequence 1351, Application US/11597825
 ; Publication No. US20090297536A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIN, Lynda
 ; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; TITLE OF INVENTION: CANCER
 ; FILE REFERENCE: DFN-059-2
 ; CURRENT APPLICATION NUMBER: US/11/597,825
 ; CURRENT FILING DATE: 2006-11-27
 ; NUMBER OF SEQ ID NOS: 1528
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1351
 ; LENGTH: 177
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-11-597-825-1351

Query Match 100.0%; Score 882; DB 7; Length 177;
 Best Local Similarity 100.0%;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5

US-12-399-906-29
 ; Sequence 29, Application US/12399906
 ; Publication No. US20100226856A1
 ; GENERAL INFORMATION
 ; APPLICANT: Vitaliano, Franco
 ; APPLICANT: Vitaliano, Gordana D
 ; TITLE OF INVENTION: DYNAMIC BIO-NANOPARTICLE ELEMENTS
 ; FILE REFERENCE: FV3011
 ; CURRENT APPLICATION NUMBER: US/12/399,906
 ; CURRENT FILING DATE: 2009-09-23
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.5
 ; SEQ ID NO 29
 ; LENGTH: 177
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: UniProtKB/P61923
 ; DATABASE ENTRY DATE: 2009-05-05
 ; RELEVANT RESIDUES IN SEQ ID NO: (1)..(177)
 US-12-399-906-29

Query Match 100.0%; Score 882; DB 8; Length 177;
 Best Local Similarity 100.0%;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLSQLRKNVEKRALLENMEG 120
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Db     61 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLSQLRKNVEKRALLENMEG 120

Qy    121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
      |||
Db    121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
  
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RESULT 6

US-11-443-428A-819804
 ; Sequence 819804, Application US/11443428A
 ; Publication No. US20070083334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mintz, Liat
 ; APPLICANT: Xie, Hanguang
 ; APPLICANT: Dahari, Dvir

```

; APPLICANT:  Levanon, Erez
; APPLICANT:  Freilich, Shiri
; APPLICANT:  Beck, Nili
; APPLICANT:  Zhu, Wei-Yong
; APPLICANT:  Wasserman, Alon
; APPLICANT:  Hermesh, Chen
; APPLICANT:  Azar, Idit
; APPLICANT:  Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819804
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819804

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Query Match          100.0%; Score 882; DB 6; Length 192;
Best Local Similarity 100.0%;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-11-443-428A-819805

; Sequence 819805, Application US/11443428A

; Publication No. US20070083334A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 819805

; LENGTH: 192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-819805

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Query Match          100.0%; Score 882; DB 6; Length 192;
Best Local Similarity 100.0%;

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Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8

US-11-443-428A-819806

; Sequence 819806, Application US/11443428A

; Publication No. US20070083334A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 819806

; LENGTH: 192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-819806

Query Match 100.0%; Score 882; DB 6; Length 192;

Best Local Similarity 100.0%;

Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEALILEPSLYTVKAILILDNDGDRLFACYDDTYPVSKQKAFKKNIFNKHRTDSEIA 60
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Db      16 MEALILEPSLYTVKAILILDNDGDRLFACYDDTYPVSKQKAFKKNIFNKHRTDSEIA 75
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Qy      61 LLEGLTVVYKSSIDLIFYFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 120
      |||
Db      76 LLEGLTVVYKSSIDLIFYFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 135
      |||

Qy      121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
      |||
Db      136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192
      |||

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RESULT 9

US-11-443-428A-819808

; Sequence 819808, Application US/11443428A

; Publication No. US20070083334A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

```

; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819808
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819808

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Query Match          100.0%; Score 882; DB 6; Length 192;
Best Local Similarity 100.0%;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVSKQKAFKFNIFNKTHTRTDSEIA 60
Db      16 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVSKQKAFKFNIFNKTHTRTDSEIA 75

Qy      61 LLEGLTVVYKSSIDLIFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 120
Db      76 LLEGLTVVYKSSIDLIFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 135

Qy      121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
Db      136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192

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RESULT 10
US-11-443-428A-819810
; Sequence 819810, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hangqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819810
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819810

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Query Match          100.0%; Score 882; DB 6; Length 192;

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Best Local Similarity      100.0%;
Matches    177;   Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRFLFAKYDDTTPSVKQEKAFEKNIFNKTHTRDSEIA 60
Db          16 MEALILEPSLYTVKAILILDNDGDRFLFAKYDDTTPSVKQEKAFEKNIFNKTHTRDSEIA 75

Qy         61 LLEGLTVVYKSSIDLIFYFYIGSSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLNMEG 120
Db         76 LLEGLTVVYKSSIDLIFYFYIGSSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLNMEG 135

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAAKEQIKWSLLR 177
Db        136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAAKEQIKWSLLR 192

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RESULT 11

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US-11-443-428A-819816
; Sequence 819816, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819816
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819816

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```

Query Match          100.0%; Score 882; DB 6; Length 192;
Best Local Similarity 100.0%;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTTPSVKQKAFEKNIFNKTHTRDSEIA 60
      |||
Db      16 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTTPSVKQKAFEKNIFNKTHTRDSEIA 75

Qy      61 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVNLCLFDSLSQMLRKNVEKRALLNMEG 120
      |||
Db      76 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVNLCLFDSLSQMLRKNVEKRALLNMEG 135

Qy      121 LFLAVDEIVDGGVILESDPQQVVRHVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
      |||
Db      136 LFLAVDEIVDGGVILESDPQQVVRHVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192

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RESULT 12

US-11-443-428A-819818
; Sequence 819818, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat


```
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819818
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819818
```

```
Query Match          100.0%; Score 882; DB 6; Length 192;
Best Local Similarity 100.0%;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MEALILEPSLYTVKAILILDNDGDRLFACYDDTYPVKEQKAFKFNPNKTHRTDSEIA 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      16 MEALILEPSLYTVKAILILDNDGDRLFACYDDTYPVKEQKAFKFNPNKTHRTDSEIA 75
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy      61 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 135
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy      121 LFLAVDEIVDGGVILESDPQQVVRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      136 LFLAVDEIVDGGVILESDPQQVVRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 13

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US-11-443-428A-819819
; Sequence 819819, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819819
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819819
```

Query Match 100.0%; Score 882; DB 6; Length 192;
 Best Local Similarity 100.0%;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEALILEPSLYTVKAILILDNDGDRLFACYDDTYPVSKQKAFKFNIFNKTHTRDSEIA 60
        |||
Db      16 MEALILEPSLYTVKAILILDNDGDRLFACYDDTYPVSKQKAFKFNIFNKTHTRDSEIA 75
        |||

Qy      61 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLNMEG 120
        |||
Db      76 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLNMEG 135
        |||

Qy      121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
        |||
Db      136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192
        |||

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RESULT 14

US-11-443-428A-819821
 ; Sequence 819821, Application US/11443428A
 ; Publication No. US20070083334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mintz, Liat
 ; APPLICANT: Xie, Hanguing
 ; APPLICANT: Dahari, Dvir
 ; APPLICANT: Levanon, Erez
 ; APPLICANT: Freilich, Shiri
 ; APPLICANT: Beck, Nili
 ; APPLICANT: Zhu, Wei-Yong
 ; APPLICANT: Wasserman, Alon
 ; APPLICANT: Hermesh, Chen
 ; APPLICANT: Azar, Idit
 ; APPLICANT: Bernstein, Jeanne
 ; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
 ; FILE REFERENCE: 02/23929
 ; CURRENT APPLICATION NUMBER: US/11/443,428A
 ; CURRENT FILING DATE: 2006-05-31
 ; NUMBER OF SEQ ID NOS: 1034312
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 819821
 ; LENGTH: 192
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-443-428A-819821

Query Match 100.0%; Score 882; DB 6; Length 192;
 Best Local Similarity 100.0%;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MEALILEPSLYTVKAILILDNDGDRLFACYDDTYPVSKQKAFKFNIFNKTHTRDSEIA 60
        |||
Db      16 MEALILEPSLYTVKAILILDNDGDRLFACYDDTYPVSKQKAFKFNIFNKTHTRDSEIA 75
        |||

Qy      61 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLNMEG 120
        |||
Db      76 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLNMEG 135
        |||

Qy      121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
        |||
Db      136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192
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RESULT 15

US-11-443-428A-819823
 ; Sequence 819823, Application US/11443428A
 ; Publication No. US20070083334A1
 ; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819823
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819823

Query Match 100.0%; Score 882; DB 6; Length 192;
Best Local Similarity 100.0%;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVKEQKAFKFNIFNKTHTDSEIA	60
Db	16	MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVKEQKAFKFNIFNKTHTDSEIA	75
Qy	61	LLEGLTVVYKSSIDLIFYFVIGSSYENELMLMAVLNCLFDSLSQLRKNVEKRALLENMEG	120
Db	76	LLEGLTVVYKSSIDLIFYFVIGSSYENELMLMAVLNCLFDSLSQLRKNVEKRALLENMEG	135
Qy	121	LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR	177
Db	136	LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR	192

Search completed: December 14, 2010, 11:32:16
Job time : 142.65 secs

SCORE 3.6

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103255_us-09-556-178-5.ra1.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103255_us-09-556-178-5.ra1.

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OM protein - protein search, using sw model

Run on: December 14, 2010, 11:24:20 ; Search time 25 Seconds
(without alignments)
2826.599 Million cell updates/sec

Title: US-09-556-178-5
Perfect score: 882
Sequence: 1 MEALILEPSLYTVKAILILD.....QTVSQVLQSAKEQIKWSLLR 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2170800 seqs, 396181022 residues

Total number of hits satisfying chosen parameters: 2170800

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
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2	882	100.0	177	2	US-09-368-408-5	Sequence 5, Appli
3	882	100.0	177	3	US-11-443-428A-819809	Sequence 819809,
4	882	100.0	192	3	US-11-443-428A-819804	Sequence 819804,
5	882	100.0	192	3	US-11-443-428A-819805	Sequence 819805,
6	882	100.0	192	3	US-11-443-428A-819806	Sequence 819806,
7	882	100.0	192	3	US-11-443-428A-819808	Sequence 819808,
8	882	100.0	192	3	US-11-443-428A-819810	Sequence 819810,
9	882	100.0	192	3	US-11-443-428A-819816	Sequence 819816,
10	882	100.0	192	3	US-11-443-428A-819818	Sequence 819818,

11	882	100.0	192	3	US-11-443-428A-819819	Sequence 819819,
12	882	100.0	192	3	US-11-443-428A-819821	Sequence 819821,
13	882	100.0	192	3	US-11-443-428A-819823	Sequence 819823,
14	882	100.0	192	3	US-11-443-428A-819825	Sequence 819825,
15	882	100.0	200	3	US-11-443-428A-819807	Sequence 819807,
16	882	100.0	205	3	US-11-443-428A-819812	Sequence 819812,
17	875	99.2	177	1	US-08-967-364-9	Sequence 9, Appli
18	875	99.2	177	2	US-09-368-408-9	Sequence 9, Appli
19	868	98.4	182	3	US-11-443-428A-819814	Sequence 819814,
20	858	97.3	172	3	US-11-443-428A-819813	Sequence 819813,
21	856	97.1	177	3	US-11-443-428A-819815	Sequence 819815,
22	856	97.1	178	3	US-11-443-428A-819811	Sequence 819811,
23	701	79.5	173	3	US-11-443-428A-819820	Sequence 819820,
24	673	76.3	214	3	US-11-443-428A-823399	Sequence 823399,
25	671	76.1	137	2	US-09-513-999C-5551	Sequence 5551, Ap
26	671	76.1	137	3	US-10-793-479-5551	Sequence 5551, Ap
27	542	61.5	134	3	US-11-443-428A-819826	Sequence 819826,
28	518	58.7	136	3	US-11-443-428A-823401	Sequence 823401,
29	510	57.8	169	3	US-11-443-428A-823406	Sequence 823406,
30	487	55.2	177	3	US-11-443-428A-819824	Sequence 819824,
31	454	51.5	138	3	US-11-443-428A-823403	Sequence 823403,
32	440	49.9	125	3	US-11-443-428A-819817	Sequence 819817,
33	360.5	40.9	95	3	US-11-443-428A-1002249	Sequence 1002249,
34	357	40.5	177	3	US-10-703-032-129014	Sequence 129014,
35	357	40.5	177	3	US-11-241-607-37572	Sequence 37572, A
36	356.5	40.4	183	3	US-10-767-701-44154	Sequence 44154, A
37	344.5	39.1	176	3	US-11-241-607-52299	Sequence 52299, A
38	340.5	38.6	176	3	US-10-767-701-39442	Sequence 39442, A
39	340	38.5	177	3	US-10-703-032-107720	Sequence 107720,
40	306.5	34.8	197	3	US-10-703-032-105938	Sequence 105938,
41	260	29.5	186	3	US-10-703-032-106783	Sequence 106783,
42	252	28.6	126	3	US-11-443-428A-819822	Sequence 819822,
43	250	28.3	97	3	US-11-443-428A-949290	Sequence 949290,
44	243	27.6	119	3	US-11-241-607-37573	Sequence 37573, A
45	228	25.9	116	3	US-10-703-032-128901	Sequence 128901,

ALIGNMENTS

RESULT 1

US-08-967-364-5

; Sequence 5, Application US/08967364

; Patent No. 5989859

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Lal, Preeti

; APPLICANT: Guegler, Karl J.

; APPLICANT: Shah, Purvi

; APPLICANT: Corley, Neil C.

; TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Dr.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/967,364

; FILING DATE: No. 598985September 7, 1997

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0417 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HEAONOT03
; CLONE: 3086794
US-08-967-364-5
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Query Match          100.0%; Score 882; DB 1; Length 177;
Best Local Similarity 100.0%;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MEALILEPSLYTVKAILILDNDGDLFAKYDDTYPVSKQKAFKFNIFNKTHTDSEIA 60
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Db      1 MEALILEPSLYTVKAILILDNDGDLFAKYDDTYPVSKQKAFKFNIFNKTHTDSEIA 60

Qy     61 LLEGLTVVYKSSIDLIFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LLEGLTVVYKSSIDLIFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 120

Qy    121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
```

```
RESULT 2
US-09-368-408-5
; Sequence 5, Application US/09368408
; Patent No. 6071703
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/368,408
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/967,364
```

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0417 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HEAONOT03
; CLONE: 3086794
US-09-368-408-5

```

```

Query Match          100.0%; Score 882; DB 2; Length 177;
Best Local Similarity 100.0%;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEALILEPSLYTVKAILILDNDGRLFAKYDDTYPVKEQKAFKFNIFNKHRTDSEIA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEALILEPSLYTVKAILILDNDGRLFAKYDDTYPVKEQKAFKFNIFNKHRTDSEIA 60

Qy     61 LLEGLTVVYKSSIDLIFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVKEKRALLNMEG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LLEGLTVVYKSSIDLIFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVKEKRALLNMEG 120

Qy     121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177

```

```

RESULT 3
US-11-443-428A-819809
; Sequence 819809, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819809
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819809

```

```

Query Match          100.0%; Score 882; DB 3; Length 177;
Best Local Similarity 100.0%;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVSKQKAFEKNIFNKTHTRDSEIA 60
      |||
Db      1 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVSKQKAFEKNIFNKTHTRDSEIA 60

Qy      61 LLEGLTVVYKSSIDLIFYVIGSSYENELMLMAVLNCLFDSLSQLMRKNVEKRALLENMEG 120
      |||
Db      61 LLEGLTVVYKSSIDLIFYVIGSSYENELMLMAVLNCLFDSLSQLMRKNVEKRALLENMEG 120

Qy      121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
      |||
Db      121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177

```

RESULT 4

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US-11-443-428A-819804
; Sequence 819804, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819804
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819804

```

```

Query Match      100.0%; Score 882; DB 3; Length 192;
Best Local Similarity 100.0%;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVSKQKAFEKNIFNKTHTRDSEIA 60
      |||
Db      16 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVSKQKAFEKNIFNKTHTRDSEIA 75

Qy      61 LLEGLTVVYKSSIDLIFYVIGSSYENELMLMAVLNCLFDSLSQLMRKNVEKRALLENMEG 120
      |||
Db      76 LLEGLTVVYKSSIDLIFYVIGSSYENELMLMAVLNCLFDSLSQLMRKNVEKRALLENMEG 135

Qy      121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
      |||
Db      136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192

```

RESULT 5

```

US-11-443-428A-819805
; Sequence 819805, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir

```



```

; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819805
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819805

```

```

Query Match          100.0%; Score 882; DB 3; Length 192;
Best Local Similarity 100.0%;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      1 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVKEQKAFAKFNIFNKTHTRDSEIA 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      16 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVKEQKAFAKFNIFNKTHTRDSEIA 75

Qy      61 LLEGLTVVYKSSIDLIFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76 LLEGLTVVYKSSIDLIFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 135

Qy      121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192

```

```

RESULT 6
US-11-443-428A-819806
; Sequence 819806, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819806
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819806

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Query Match          100.0%; Score 882; DB 3; Length 192;
Best Local Similarity 100.0%;

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Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVSKQKAFKKNIFNKHRTDSEIA 60
      |||
Db      16 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVSKQKAFKKNIFNKHRTDSEIA 75
      |||

Qy      61 LLEGLTVVYKSSIDLIFYFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 120
      |||
Db      76 LLEGLTVVYKSSIDLIFYFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 135
      |||

Qy      121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
      |||
Db      136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192
      |||

```

RESULT 7

US-11-443-428A-819808

; Sequence 819808, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 819808

; LENGTH: 192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-819808

Query Match 100.0%; Score 882; DB 3; Length 192;

Best Local Similarity 100.0%;

Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVSKQKAFKKNIFNKHRTDSEIA 60
      |||
Db      16 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVSKQKAFKKNIFNKHRTDSEIA 75
      |||

Qy      61 LLEGLTVVYKSSIDLIFYFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 120
      |||
Db      76 LLEGLTVVYKSSIDLIFYFYVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 135
      |||

Qy      121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
      |||
Db      136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192
      |||

```

RESULT 8

US-11-443-428A-819810

; Sequence 819810, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

```

; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819810
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819810

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Query Match          100.0%; Score 882; DB 3; Length 192;
Best Local Similarity 100.0%;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MEALILEPSLYTVKAILILDNDGDLFAKYDDTYPVSKQKAFKFNIFNKTHTRTDSEIA 60
Db      16 MEALILEPSLYTVKAILILDNDGDLFAKYDDTYPVSKQKAFKFNIFNKTHTRTDSEIA 75
      |||
Qy      61 LLEGLTVVYKSSIDLIFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 120
Db      76 LLEGLTVVYKSSIDLIFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG 135
      |||
Qy      121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
Db      136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192
      |||

```

RESULT 9

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US-11-443-428A-819816
; Sequence 819816, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanguing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819816
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819816

```

```

Query Match          100.0%; Score 882; DB 3; Length 192;

```



```
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819819
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819819
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Query Match          100.0%; Score 882; DB 3; Length 192;
Best Local Similarity 100.0%;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MEALILEPSLYTVKAILILDNDGDRLFACYDDTYPVKEQKAFKFNPNKTHRTDSEIA 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      16 MEALILEPSLYTVKAILILDNDGDRLFACYDDTYPVKEQKAFKFNPNKTHRTDSEIA 75
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy      61 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 135
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy      121 LFLAVDEIVDGGVILESDPQQVVRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      136 LFLAVDEIVDGGVILESDPQQVVRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 12

```
US-11-443-428A-819821
; Sequence 819821, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819821
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819821
```

Query Match 100.0%; Score 882; DB 3; Length 192;
 Best Local Similarity 100.0%;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEALILEPSLYTVKAILILDNDGDRLFACYDDTYPVSVEKQKAFKFNIFNKTHTRDSEIA 60
 |||
 Db 16 MEALILEPSLYTVKAILILDNDGDRLFACYDDTYPVSVEKQKAFKFNIFNKTHTRDSEIA 75
 |||
 Qy 61 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLNMEG 120
 |||
 Db 76 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLNMEG 135
 |||
 Qy 121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVS QVLQSAKEQIKWSLLR 177
 |||
 Db 136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVS QVLQSAKEQIKWSLLR 192
 |||

RESULT 13

US-11-443-428A-819823

; Sequence 819823, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanguing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 819823

; LENGTH: 192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-819823

Query Match 100.0%; Score 882; DB 3; Length 192;
 Best Local Similarity 100.0%;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEALILEPSLYTVKAILILDNDGDRLFACYDDTYPVSVEKQKAFKFNIFNKTHTRDSEIA 60
 |||
 Db 16 MEALILEPSLYTVKAILILDNDGDRLFACYDDTYPVSVEKQKAFKFNIFNKTHTRDSEIA 75
 |||
 Qy 61 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLNMEG 120
 |||
 Db 76 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLNMEG 135
 |||
 Qy 121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVS QVLQSAKEQIKWSLLR 177
 |||
 Db 136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVS QVLQSAKEQIKWSLLR 192
 |||

RESULT 14

US-11-443-428A-819825

; Sequence 819825, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

```
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819825
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819825
```

```
Query Match          100.0%; Score 882; DB 3; Length 192;
Best Local Similarity 100.0%;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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Qy      1 MEALILEPSLYTVKAILILDNDGDRLFAKYDDTYPVKEQKAFKFNKTHRTDSEIA 60
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Qy      61 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
Db      76 LLEGLTVVYKSSIDLYFYFVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 135

Qy      121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
Db      136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192
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RESULT 15

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; Sequence 819807, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819807
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-819807
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Query Match 100.0%; Score 882; DB 3; Length 200;
 Best Local Similarity 100.0%;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	LLEGLTVVYKSSIDLIFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG	120
Db	84	LLEGLTVVYKSSIDLIFYFVIGSSYENELMLMAVLNCLFDSLQMLRKNVEKRALLENMEG	143
Qy	121	LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR	177
Db	144	LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR	200

Search completed: December 14, 2010, 11:25:12
 Job time : 24.8086 secs

SCORE 3 0

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103257_us-09-556-178-5.rapbn.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103257_us-09-556-178-5.rapbn.

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OM protein - protein search, using sw model

Run on: December 14, 2010, 11:32:21 ; Search time 1 Seconds
(without alignments)
1087.643 Million cell updates/sec

Title: US-09-556-178-5
Perfect score: 882
Sequence: 1 MEALILEPSLYTVKAILILD.....QTVSQVLQSAKEQIKWSLLR 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 23285 seqs, 2931653 residues

Total number of hits satisfying chosen parameters: 23285

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /ABSS/Data/CRF/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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3: /ABSS/Data/CRF/ptodata/2/pubpaa/US12_NEW_PUB.pep:*
SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	74.5	8.4	379	3	US-12-800-898-1740	Sequence 1740, Ap
2	74	8.4	1297	3	US-12-781-078-7	Sequence 7, Appli
3	74	8.4	1297	3	US-12-781-099-7	Sequence 7, Appli
4	74	8.4	1297	3	US-12-781-106-7	Sequence 7, Appli
5	74	8.4	1297	3	US-12-781-113-7	Sequence 7, Appli
6	74	8.4	1297	3	US-12-781-126-7	Sequence 7, Appli
7	74	8.4	1297	3	US-12-781-216-7	Sequence 7, Appli
8	74	8.4	1297	3	US-12-781-244-7	Sequence 7, Appli
9	74	8.4	1297	3	US-12-781-261-7	Sequence 7, Appli
10	74	8.4	1297	3	US-12-781-284-7	Sequence 7, Appli
11	72.5	8.2	872	3	US-12-523-023-1	Sequence 1, Appli
12	71	8.0	788	3	US-12-739-689-55	Sequence 55, Appl
13	71	8.0	1979	3	US-12-739-689-47	Sequence 47, Appl
14	71	8.0	1979	3	US-12-739-723-41	Sequence 41, Appl

15	68	7.7	517	3	US-12-783-952-168	Sequence 168, App
16	67.5	7.7	1034	3	US-12-797-443-569	Sequence 569, App
17	67.5	7.7	1053	3	US-12-797-443-568	Sequence 568, App
18	67.5	7.7	1054	3	US-12-797-443-573	Sequence 573, App
19	67.5	7.7	1057	3	US-12-797-443-567	Sequence 567, App
20	67.5	7.7	1081	3	US-12-797-443-566	Sequence 566, App
21	67	7.6	285	3	US-12-625-053A-57	Sequence 57, Appl
22	67	7.6	297	3	US-12-800-898-2856	Sequence 2856, Ap
23	67	7.6	2325	3	US-12-739-689-28	Sequence 28, Appl
24	67	7.6	2325	3	US-12-739-723-30	Sequence 30, Appl
25	66.5	7.5	863	3	US-12-682-544-19	Sequence 19, Appl
26	66.5	7.5	1274	3	US-12-781-078-6	Sequence 6, Appli
27	66.5	7.5	1274	3	US-12-781-099-6	Sequence 6, Appli
28	66.5	7.5	1274	3	US-12-781-106-6	Sequence 6, Appli
29	66.5	7.5	1274	3	US-12-781-113-6	Sequence 6, Appli
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36	65.5	7.4	524	3	US-12-599-679-9	Sequence 9, Appli
37	65.5	7.4	1086	3	US-12-800-898-3614	Sequence 3614, Ap
38	64.5	7.3	128	3	US-12-800-898-2126	Sequence 2126, Ap
39	64.5	7.3	466	3	US-12-800-898-4120	Sequence 4120, Ap
40	64	7.3	315	3	US-12-800-898-3186	Sequence 3186, Ap
41	64	7.3	341	3	US-12-713-239-93	Sequence 93, Appl
42	63.5	7.2	352	3	US-12-086-571-57	Sequence 57, Appl
43	63.5	7.2	438	3	US-12-800-898-3508	Sequence 3508, Ap
44	63.5	7.2	519	3	US-12-671-898-61	Sequence 61, Appl
45	63.5	7.2	524	3	US-12-599-679-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-12-800-898-1740

; Sequence 1740, Application US/12800898

; Publication No. US20100303822A1

; GENERAL INFORMATION:

; APPLICANT: MASIGNANI, Vega

; APPLICANT: ARICO, Maria

; TITLE OF INVENTION: POLYPEPTIDES FROM NON-TYPEABLE HAEMOPHILUS INFLUENZAE

; FILE REFERENCE: PP022930.0003

; CURRENT APPLICATION NUMBER: US/12/800,898

; CURRENT FILING DATE: 2010-05-25

; PRIOR APPLICATION NUMBER: US/11/596,557

; PRIOR FILING DATE: 2006-11-14

; PRIOR APPLICATION NUMBER: GB-0410866.8

; PRIOR FILING DATE: 2004-05-14

; NUMBER OF SEQ ID NOS: 5095

; SOFTWARE: SeqWin99, version 1.0.4

; SEQ ID NO 1740

; LENGTH: 379

; TYPE: PRT

; ORGANISM: Haemophilus influenzae

; FEATURE:

; OTHER INFORMATION: Name: NTH0958

US-12-800-898-1740

Query Match 8.4%; Score 74.5; DB 3; Length 379;

Best Local Similarity 23.2%;

Matches 46; Conservative 34; Mismatches 63; Indels 55; Gaps 10;

Qy 8 PSLYTVKAILLDN-----DGDRL----FAKYDDTYSVKEQKAFKNI--FNKT-- 52

|:| | |: :: | | | | | : | : | | | | |: :: | :: |